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OM protein - protein search, using sw model

Run on: February 4, 2003, 20:56:03 ; Search time 40 Seconds
(without alignments)
709.828 Million cell updates/sec

Title: US-09-677-752-2

Perfect score: 5086

Sequence: 1 MKKAFFFLIGNSLGLARE.....GFYSSSTFCNYLNGELALRF 965

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents_AA:*

- 1: /cgn2.6/ptodata/2/iaa/5A_COMB.pep.*
- 2: /cgn2.6/ptodata/2/iaa/5B_COMB.pep.*
- 3: /cgn2.6/ptodata/2/iaa/6A_COMB.pep.*
- 4: /cgn2.6/ptodata/2/iaa/6B_COMB.pep.*
- 5: /cgn2.6/ptodata/2/iaa/PCTUS_COMB.pep.*
- 6: /cgn2.6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4994.5	98.2	964	4	US-09-556-877-177
2	4994.5	98.2	964	4	US-09-620-412C-177
3	4919.5	96.7	977	4	US-09-556-877-191
4	4919.5	96.7	977	4	US-09-620-412C-191
5	647	12.7	982	4	US-09-556-877-176
6	647	12.7	982	4	US-09-620-412C-176
7	647	12.7	1006	4	US-09-556-877-190
8	647	12.7	1006	4	US-09-620-412C-190
9	605.5	11.9	715	4	US-09-620-412C-321
10	471.5	9.3	880	4	US-09-556-877-175
11	471.5	9.3	880	4	US-09-620-412C-175
12	459.5	9.0	866	4	US-09-556-877-189
13	459.5	9.0	866	4	US-09-620-412C-189
14	398.5	7.8	1752	4	US-09-556-877-180
15	398.5	7.8	1752	4	US-09-620-412C-180
16	386.5	7.6	1530	4	US-09-556-877-178
17	386.5	7.6	1530	4	US-09-620-412C-178
18	371.5	7.3	715	4	US-09-620-412C-329
19	365	7.2	848	4	US-09-556-877-192
20	365	7.2	848	4	US-09-620-412C-192
21	363	7.1	1776	4	US-09-556-877-179
22	363	7.1	1776	4	US-09-620-412C-179
23	345.5	6.8	948	4	US-09-556-877-194
24	345.5	6.8	948	4	US-09-620-412C-194
25	340	6.7	646	4	US-09-620-412C-317
26	320.5	6.3	691	4	US-09-620-412C-313
27	278.5	5.5	631	4	US-09-620-412C-325

28	246.5	4.8	619	4	US-09-620-412C-309
29	235	4.6	700	4	US-09-620-412C-345
30	221.5	4.4	821	4	US-09-556-877-195
31	221.5	4.4	821	4	US-09-620-412C-195
32	220.5	4.3	654	4	US-09-620-412C-341
33	215	4.2	778	4	US-09-556-877-193
34	215	4.2	778	4	US-09-620-412C-193
35	205	4.0	683	4	US-09-620-412C-357
36	194	3.8	1612	1	US-08-169-927-2
37	192.5	3.8	1095	4	US-09-206-942-45
38	192.5	3.8	1101	4	US-09-206-942-43
39	188.5	3.7	583	4	US-09-620-412C-353
40	181.5	3.6	915	4	US-09-206-942-35
41	181.5	3.6	1222	4	US-09-206-942-37
42	181.5	3.6	1228	4	US-09-206-942-34
43	177.5	3.5	1338	2	US-08-728-470-9
44	177.5	3.5	1338	4	US-08-719-641-9
45	177.5	3.5	1599	2	US-08-617-697-9

ALIGNMENTS

RESULT 1
US-09-556-877-177
; Sequence 177, Application US/09556877
; Patent No. 6,432,916
; GENERAL INFORMATION:
; APPLICANT: Probst, Peter
; APPLICANT: Bhatia, Ajay
; APPLICANT: Skeiky, Yasir
; APPLICANT: Flings, Steve
; APPLICANT: Maisonneuve, Jeff
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
; FILE REFERENCE: 210121.469C5
; CURRENT APPLICATION NUMBER: US/09/556,877
; CURRENT FILING DATE: 2000-04-19
; NUMBER OF SEQ ID NOS: 305
; SOFTWARE: FastSeq for Windows Version 3.0/4.0
; SEQ ID NO 177
; LENGTH: 964
; TYPE: PRT
; ORGANISM: Chlamydia
US-09-556-877-177

Query Match	98.2%	Score 4994.5;	DB 4;	Length 964;
Best Local Similarity	98.4%	Pred. No. 0;		
Matches	950;	Conservative	7;	Mismatches 1;
Gaps	1;			
QY	1	MKKAFFFLIGNSLGLAREVPSRIFLMPNSVDPPTKESLSNKISLTGDTHTNLTNCYLDN	60	
Db	1	MKKAFFFLIGNSLGLAREVPSRIFLMPNSVDPPTKESLSNKISLTGDTHTNLTNCYLDN	60	
QY	61	LRYLALQKTPREGAAVTITDYLSPFDKQEGIFYAKNLTPESSGAIGVASNPSPIVEI	120	
Db	61	LRYLALQKTPREGAAVTITDYLSPFDKQEGIFYAKNLTPESSGAIGVASNPSPIVEI	120	
QY	121	RDITGPVIFENNCCRRPFTSSNPNAAVNKIREGAIHAQNLYNHNHNDVYGVFMKNFSYVR	180	
Db	121	RDITGPVIFENNCCRRPFTSSNPNAAVNKIREGAIHAQNLYNHNHNDVYGVFMKNFSYVR	180	
QY	181	GGAIstantantvwsenoscflfmdnncicqtnntagkgaiyagtsnpsfenncdlffinnac	239	
Db	181	GGAIstantantvwsenoscflfmdnncicqtnntagkgaiyagtsnpsfenncdlffinnac	239	
QY	241	CAGAIstfpcsttgnrnlvfyvnnrcfknvettassdggatkvttrldvtngrgrif	300	
Db	241	CAGAIstfpcsttgnrnlvfyvnnrcfknvettassdggatkvttrldvtngrgrif	300	
QY	301	FSDNITKNYGAIIYAPVVTTLVDNGPTYFINNIANNKGAIYIDGTSNKSISADRHAIIFN	360	
Db	301	FSDNITKNYGAIIYAPVVTTLVDNGPTYFINNIANNKGAIYIDGTSNKSISADRHAIIFN	360	
QY	359	FSDNITKNYGAIIYAPVVTTLVDNGPTYFINNIANNKGAIYIDGTSNKSISADRHAIIFN	359	
Db	359	FSDNITKNYGAIIYAPVVTTLVDNGPTYFINNIANNKGAIYIDGTSNKSISADRHAIIFN	359	

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QY 361 ENIVNTNANGTSTSANPPRRNAITVASSGSEILLGAGSSONLIFYDPIEVSNAGVSYS 420
|||||
Db 360 ENIVNTNANGTSTSANPPRRNAITVASSGSEILLGAGSSONLIFYDPIEVSNAGVSYS 419
|||||
QY 421 FNKEADQSGVVSFGATVNSADFHORNLOTKTPAPLTLNSGFLCIEDHAQLTVNRFTQTG 480
|||||
Db 420 FNKEADQSGVVSFGATVNSADFHORNLOTKTPAPLTLNSGFLCIEDHAQLTVNRFTQTG 479
|||||
QY 481 GVSILGNAGVLSKYKNGAGNSASNASITLKHIGLNLSSILKSGAETPLLWVEPTNNSNY 540
|||||
Db 480 GVSILGNAGVLSKYKNGAGNSASNASITLKHIGLNLSSILKSGAETPLLWVEPTNNSNY 539
|||||
QY 541 TADTAATFSLSDVKLSLDDYGNPSYESTDLTHALSSOPMLISSEASDNQDSEIDFSG 600
|||||
Db 540 TADTAATFSLSDVKLSLDDYGNPSYESTDLTHALSSOPMLISSEASDNQDSEIDFSG 599
|||||
QY 601 LNVPHYGWGLTWGWAQTQDPEPASATITDPOKANRFRHTLLTLWLPAGVYVSPKHS 660
|||||
Db 600 LNVPHYGWGLTWGWAQTQDPEPASATITDPOKANRFRHTLLTLWLPAGVYVSPKHS 659
|||||
QY 661 PLIANTLWGNMLLATESLKNSEALTPSGHPFWGITGGGLGMVYQDPRENHPGFHMRSSG 720
|||||
Db 660 PLIANTLWGNMLLATESLKNSEALTPSGHPFWGITGGGLGMVYQDPRENHPGFHMRSSG 719
|||||
QY 721 YSAGMIAGOTHTFSLKFSOTYTKLNERAKNNVSSKNYSCQEMLFSLOEGFLTLKVL 780
|||||
Db 720 YSAGMIAGOTHTFSLKFSOTYTKLNERAKNNVSSKNYSCQEMLFSLOEGFLTLKVL 779
|||||
QY 781 YSYGDHCHHFYTOGENLTSGTFRSQTMGGAVFDDLPKPGSTHILTAFLGALGIYS 840
|||||
Db 780 YSYGDHCHHFYTOGENLTSGTFRSQTMGGAVFDDLPKPGSTHILTAFLGALGIYS 839
|||||
QY 841 SLSHFTEVGAYPRSFSTKTPLINVLPIGVKGSFNNATQPOAWTVELAYQVLYRQEPG 900
|||||
Db 840 SLSHFTEVGAYPRSFSTKTPLINVLPIGVKGSFNNATQPOAWTVELAYQVLYRQEPG 899
|||||
QY 901 IATOLLASKGIWFGSGSPSSRHAMSYSKISQOTQPLSWLTLHFQYHGFYSSTFCNYLNGE 960
|||||
Db 900 IATOLLASKGIWFGSGSPSSRHAMSYSKISQOTQPLSWLTLHFQYHGFYSSTFCNYLNGE 959
|||||
QY 961 IALRF 965
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Db 960 IALRF 964
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RESULT 2

US-09-620-412C-177

; Sequence 177, Application US/09620412C

; Patent No. 6448834

; GENERAL INFORMATION:

; APPLICANT: Steven P. Fling

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND

; TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION

; FILE REFERENCE: 210121.469C7

; CURRENT APPLICATION NUMBER: US/09/620.412C

; CURRENT FILING DATE: 2000-07-20

; NUMBER OF SEQ ID NOS: 363

; SOFTWARE: FastSeq for Windows Version 3.0/4.0

; SEQ ID NO 177

; LENGTH: 964

; TYPE: PRN

; ORGANISM: Chlamydia

US-09-620-412C-177

Query Match

Best Local Similarity 98.2%; Score 4994.5; DB 4; Length 964;

Matches 950; Conservative 7; Mismatches 7; Indels 1; Gaps 1;

QY 1 MKKAFFFLIGNSLGLAREVPSRIFLMPNSVPDPTKESLKNKISLTGDTNLTNCYLDN 60

Db 1 MKKAFFFLIGNSLGLAREVPSRIFLMPNSVPDPTKESLKNKISLTGDTNLTNCYLDN 60

```
; APPLICANT: Fling, Steve
; APPLICANT: Maisonneuve, Jeff
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
; FILE REFERENCE: 210121.469C5
; CURRENT APPLICATION NUMBER: US/09/556,877
; CURRENT FILING DATE: 2000-04-19
; NUMBER OF SEQ ID NOS: 305
; SOFTWARE: FastSeq for Windows Version 3.0/4.0
; SEQ ID NO 191
; LENGTH: 977
; TYPE: PRT
; ORGANISM: Chlamydia
US-09-556-877-191

Query Match          96.7%; Score 4919.5; DB 4; Length 977;
Best Local Similarity 98.4%; Pred. No. 0;
Matches 935; Conservative 7; Mismatches 7; Indels 1; Gaps 1;

QY 16 GLAREVPSRIFLMPNSVPDPTKESLSNKISLTGTHNLTCYLDNLRYILAILOKTPNEG 75
Db 29 GLAREVPSRIFLMPNSVPDPTKESLSNKISLTGTHNLTCYLDNLRYILAILOKTPNEG 88
QY 76 AAVTITDLSFFDQKEGIYFAKNLTPESGGAIGYASPNSTVEIRDTIGPVIFENNTCC 135
Db 89 AAVTITDLSFFDQKEGIYFAKNLTPESGGAIGYASPNSTVEIRDTIGPVIFENNTCC 148
QY 136 RPTSSNPNAVNKIRREGGAIHAQNLINHNHVVGVGPMKNFSYVGGAIANTFVYSEN 195
Db 149 RLFTWRNPYAA-DKIRREGGAIHAQNLINHNHVVGVGPMKNFSYVGGAIANTFVYSEN 207
QY 196 QSCFLFMDNICIQNTAGKGAIIYAGTNSFESNNCDLFFINNACCAGGAIFSPICSLTG 255
Db 208 QSCFLFMDNICIQNTAGKGAIIYAGTNSFESNNCDLFFINNACCAGGAIFSPICSLTG 267
QY 256 NRGNIVFYNNRCFKNVETASSEASDGGAIKVTTRLDVTGNRGIFFSDNITKNYGGAIYA 315
Db 268 NRGNIVFYNNRCFKNVETASSEASDGGAIKVTTRLDVTGNRGIFFSDNITKNYGGAIYA 327
QY 316 PVTLVDNGPTYFNNIANKKGAIYIDGTSNKSISADRAHAIIFENIVNTNANGTST 375
Db 328 PVTLVDNGPTYFNNIANKKGAIYIDGTSNKSISADRAHAIIFENIVNTNANGTST 387
QY 376 SANPPRNAITVASSSGEILLGAGSSQNLIFYDPIEVSNAGVSVPFNKEADQTSVVFSG 435
Db 388 SANPPRNAITVASSSGEILLGAGSSQNLIFYDPIEVSNAGVSVPFNKEADQTSVVFSG 447
QY 436 ATVNSADFHORNLOTKTPAPLTLNSGFLCTIEDHAQLTVNRFRTQTGGVYSLGNGAVLSYK 495
Db 508 NGTGDASNASITLKHIGLNLSSLLKSGAEIPLLWVEPTNNSNNYTADTAATFSLSDVKL 567
QY 556 SLIDDYGNPSYESTDLTHALSSQPMLSISEASDNLQSDDDFSLGNVPHYGWGLWTWG 615
Db 568 SLIDDYGNPSYESTDLTHALSSQPMLSISEASDNLQSDDDFSLGNVPHYGWGLWTWG 627
QY 616 WAKTQDPEPASSATITDQKARNRPHRTLLTLWLPAGYVPSPKRSPLIANTLWGNMLLAT 675
Db 628 WAKTQDPEPASSATITDQKARNRPHRTLLTLWLPAGYVPSPKRSPLIANTLWGNMLLAT 687
QY 676 ESLKNSAELTPSDHPFWGITGGGLGMVYQDPPRENHPGFHMRSSGYSGAGIAGTHTFSL 735
Db 688 ESLKNSAELTPSDHPFWGITGGGLGMVYQDPPRENHPGFHMRSSGYSGAGIAGTHTFSL 747
QY 736 KFSQTYTKLERYAKNNVSKNTSCQGEMLFSLQEGFLTLKVLGYSGDHNCHHFTQG 795
Db 748 KFSQTYTKLERYAKNNVSKNTSCQGEMLFSLQEGFLTLKVLGYSGDHNCHHFTQG 807
QY 796 ENLTSQGTFRSOTMGGAVFFDLPMKPFGSTHILTAFLGALGIYSSLSHTEVGAYPRSF 855
Db 855 ENLTSQGTFRSOTMGGAVFFDLPMKPFGSTHILTAFLGALGIYSSLSHTEVGAYPRSF 867
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Db 808 ENLTSQGTFRSOTMGGAVFFDLPMKPFGSTHILTAFLGALGIYSSLSHTEVGAYPRSF 867
QY 856 STKTPLINLVPIGVKGSFNMATOPQAWTVLAYQVLYRQEPGIATQLLASKGIWFGS 915
Db 868 STKTPLINLVPIGVKGSFNMATOPQAWTVLAYQVLYRQEPGIATQLLASKGIWFGS 927
QY 916 GSPSSRHAMSYSKISQQTQPLSWLTLHFQYHGFYSSTFCNLYLNGEIALRF 965
Db 928 GSPSSRHAMSYSKISQQTQPLSWLTLHFQYHGFYSSTFCNLYLNGEIALRF 977

RESULT 4
US-09-620-412C-191
; Sequence 191, Application US/09620412C
; Patent No. 6448234
; GENERAL INFORMATION:
; APPLICANT: Steven P. Fling
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
; FILE REFERENCE: 210121.469C7
; CURRENT APPLICATION NUMBER: US/09/620,412C
; CURRENT FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 363
; SOFTWARE: FastSeq for Windows Version 3.0/4.0
; SEQ ID NO 191
; LENGTH: 977
; TYPE: PRT
; ORGANISM: Chlamydia
US-09-620-412C-191
```

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Query Match          96.7%; Score 4919.5; DB 4; Length 977;
Best Local Similarity 98.4%; Pred. No. 0;
Matches 935; Conservative 7; Mismatches 7; Indels 1; Gaps 1;

QY 16 GLAREVPSRIFLMPNSVPDPTKESLSNKISLTGTHNLTCYLDNLRYILAILOKTPNEG 75
Db 29 GLAREVPSRIFLMPNSVPDPTKESLSNKISLTGTHNLTCYLDNLRYILAILOKTPNEG 88
QY 76 AAVTITDLSFFDQKEGIYFAKNLTPESGGAIGYASPNSTVEIRDTIGPVIFENNTCC 135
Db 89 AAVTITDLSFFDQKEGIYFAKNLTPESGGAIGYASPNSTVEIRDTIGPVIFENNTCC 148
QY 136 RPTSSNPNAVNKIRREGGAIHAQNLINHNHVVGVGPMKNFSYVGGAIANTFVYSEN 195
Db 149 RLFTWRNPYAA-DKIRREGGAIHAQNLINHNHVVGVGPMKNFSYVGGAIANTFVYSEN 207
QY 196 QSCFLFMDNICIQNTAGKGAIIYAGTNSFESNNCDLFFINNACCAGGAIFSPICSLTG 255
Db 208 QSCFLFMDNICIQNTAGKGAIIYAGTNSFESNNCDLFFINNACCAGGAIFSPICSLTG 267
QY 256 NRGNIVFYNNRCFKNVETASSEASDGGAIKVTTRLDVTGNRGIFFSDNITKNYGGAIYA 315
Db 268 NRGNIVFYNNRCFKNVETASSEASDGGAIKVTTRLDVTGNRGIFFSDNITKNYGGAIYA 327
QY 316 PVTLVDNGPTYFNNIANKKGAIYIDGTSNKSISADRAHAIIFENIVNTNANGTST 375
Db 328 PVTLVDNGPTYFNNIANKKGAIYIDGTSNKSISADRAHAIIFENIVNTNANGTST 387
QY 376 SANPPRNAITVASSSGEILLGAGSSQNLIFYDPIEVSNAGVSVPFNKEADQTSVVFSG 435
Db 388 SANPPRNAITVASSSGEILLGAGSSQNLIFYDPIEVSNAGVSVPFNKEADQTSVVFSG 447
QY 436 ATVNSADFHORNLOTKTPAPLTLNSGFLCTIEDHAQLTVNRFRTQTGGVYSLGNGAVLSYK 495
Db 448 ATVNSADFHORNLOTKTPAPLTLNSGFLCTIEDHAQLTVNRFRTQTGGVYSLGNGAVLSYK 507
QY 496 NGAGNSASNASITLKHIGLNLSSLLKSGAEIPLLWVEPTNNSNNYTADTAATFSLSDVKL 555
Db 508 NGTGDASNASITLKHIGLNLSSLLKSGAEIPLLWVEPTNNSNNYTADTAATFSLSDVKL 567
QY 556 SLIDDYGNPSYESTDLTHALSSQPMLSISEASDNLQSDDDFSLGNVPHYGWGLWTWG 615
Db 568 SLIDDYGNPSYESTDLTHALSSQPMLSISEASDNLQSDDDFSLGNVPHYGWGLWTWG 627
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Qy	616	WAKTQDPEPASSATITDPQKANRFRHTLLLTWLPAGYVSPKHRSPLIANTLWGNMLLAT	675
Db	628	WAKTQDPEPASSATITDPQKANRFRHTLLLTWLPAGYVSPKHRSPLIANTLWGNMLLAT	687
Qy	676	ESLKSNAELTPSDHPFWGITGGGLGMWYQDPRNHPGFHMSSGYSAGMIAGQHTFTSL	735
Db	688	ESLKSNAELTPSGHPFWGITGGGLGMWYQDPRNHPGFHMSSGYSAGMIAGQHTFTSL	747
Qy	736	KFSQTYTKLNERYAKNNVSSKNYSCOGEMLFSLQEGFLTLKVLGYSYGDHNCHEFTQG	795
Db	748	KFSQTYTKLNERYAKNNVSSKNYSCOGEMLFSLQEGFLTLKVLGYSYGDHNCHEFTQG	807
Qy	796	ENLTSGTFRSQTMGGAVFEDLPKMPFGSTHIIITAPFLGALGIYSSLSHFTVEVGAYPRSF	855
Db	808	ENLTSGTFRSQTMGGAVFEDLPKMPFGSTHIIITAPFLGALGIYSSLSHFTVEVGAYPRSF	867
Qy	856	STKTPLINLVLPVIGVKGSFMNATQRQAWTVELAYQPVLYRQEPGIATOLLASKGIWFGS	915
Db	868	STKTPLINLVLPVIGVKGSFMNATQRQAWTVELAYQPVLYRQEPGIATOLLASKGIWFGS	927
Qy	916	GPSSSRRHMSYKISQQTQPLSWLTLHFQYHGFGYSSSTFCNYLNGEIALRF	965
Db	928	GPSSSRRHMSYKISQQTQPLSWLTLHFQYHGFGYSSSTFCNYLNGEIALRF	977
RESULT 5			
US-09-556-877-176			
; Sequence 176, Application US/09556877			
; Patent No. 6432916			
; GENERAL INFORMATION:			
; APPLICANT: Probst, Peter			
; APPLICANT: Bhatia, Ajay			
; APPLICANT: Skeiky, Yasir			
; APPLICANT: Fling, Steve			
; APPLICANT: Maisonneuve, Jeff			
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND			
; TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION			
; FILE REFERENCE: 210121.469C5			
; CURRENT APPLICATION NUMBER: US/09/556,877			
; CURRENT FILING DATE: 2000-04-19			
; NUMBER OF SEQ ID NOS: 305			
; SOFTWARE: FastSeq for Windows Version 3.0/4.0			
; SEQ ID NO 176			
; LENGTH: 982			
; TYPE: PRT			
; ORGANISM: Chlamydia			
; FEATURE:			
; NAME/KEY: VARIANT			
; LOCATION: (1)...(982)			
; OTHER INFORMATION: xaa = Any Amino Acid			
US-09-556-877-176			

Qy	244	GATFSPICSLTGNRGNIVFYNN--RCFKN-----VETASEASDGGAI	284
		: :	
Db	259	GGIYS-----YGVAFELNGKTLFLNNVASPVYIAAKQPTSGOASNTSNNYGDGGA	310
		: :	
Qy	285	KVTTRLDVTGN-----RGRIEFSDNITKNYGAIAPVVLVDNGPTVFINNANN	335
		: : : : :	
Db	311	FCKGAQAAGNSGSVSFDGEVVFFSSNVAAKGGAITYAKKLVSANCPOVQLRNAND	370
		: : : : :	
Qy	336	KGAIYIDGTNSKISADRHAIIFNEI-----VTNVTNANGSTSANPPRNAITVASSS	391
		: : : : : : : :	
Db	371	-GGAIYLGESEGLSLSADYCDIIFDGNLKTAKENAADVNGVTSS----QAISMGG	424
		: : : : : : : : : : : : : : :	
Qy	392	GEILLGAGSSONLIFYDPIEVSN-----AGVSYSFNKEADOTGSWFESGATVNSADPH	444
		: : : : : : : : : : : : : : :	
Db	425	KITTLRAKAGHQILFNDPITEMANGNOPAQOSSKLLKINDGEGYTDIVFAN---GSSTLY	481
		: : : : : : : : : : : : : : :	
Qy	445	QRNLQTKTPAPLTSLNSGFLCIEDHQAOLTYNRFTQTGGVYSLNGAVLSCKNCAGNS--A	502
		: : : : : : : : : : : : : : :	
Db	482	QN-----VTIEGRIVRLREKAKLSVNSJSTGGSLMEAGSTLDFVTPQPQQPPA	532
		: : : : : : : : : : : : : : :	
Qy	503	SNASITLKHLGLNLSLISKSGAEIPLLWPEPTN--NSNNYTADTAATFSLSDVKLS--L	557
		: : : : : : :	
Db	533	ANQLITLSNLHLSSLALLANA-----VTNPPTNPQAQDSHPAIGST-TAGSVTTSGPFI	587
		: : : : : : :	
Qy	558	IDDYGNSPYESTD-----LTHALSSQPMLSISEASDQLRSDDDMFSLGNVPHYG	607
		: : : : : : : : : : : : : : :	
Db	588	FEDLDDTAYDRYDWLGWSNQKINVKLQLGTHKP--PANAPSDLTL-----GNEMPKVG	637
		: : : : : : : : : : : : : : :	
Qy	608	WOGLWTWGWAKTODPEPASATITDQKANRRHTLLLTLWPAGYVPSPKHRSPLIANPL	667
		: : : : : : :	
Db	638	YOGSWKLAW-----DPNTANNGPYTLKATWTKTGYNPGPERVASLPVNSL	682
		: : : : : : : : : : : : : : :	
Qy	668	WGNMLLATSLKNSAELTPSDHPFW-GITGGGLGMVMYODPRENHGPHRMSGYSAGMI	726
		: : : : : : : : : : : : : :	
Db	683	WGS-ILDIRSAHAQASVDGRSYCRGLWMVGSNFYYHDRDALGOGYRYISGGYSLG--	739
		: : : : : : : : : : : : : : :	
Qy	727	AGOTHFTSLKFSOTYTKLNERYAKNNV--SSKNYSCEGEMLFSLQEGFLTLLKLVGLYSYG	784
		: : : : : : : : : : : : : : :	
Db	740	-ANSYFGSSMFLAFTVEGFR-SKDYVVCRSNHACIGSVYLSLTOQA-----LCGSYLEG	792
		: : : : : : : : : : : : : : :	
Qy	785	DHNCHPYTGQ-ENLTSQGTFRSQT-----MGAVFPDLPMKPFPGSTHILT--APPL	833
		: : : : : : : : : : : : : : :	
Db	793	DAFIRASYGFNGHMKTSYTFABESDVVRWDNNCLAGEIGAAGLPVITTPSKLYLNELRPV	852
		: : : : : : : : : : : : : : :	
Qy	834	GALGIYSSLSHFTVEGAYPRSESTKPTLINVLVPYGVKGSFNNATORQOAWTELAYQPV	893
		: : : : : : : : : : : : : : :	
Db	853	QAREFSADHESFTEEGDQARAFKS-CHLLNLVSPVGVKFDRCSST-HPNKYSFMAYICD	910
		: : : : : : : : : : : : :	
Qy	894	LYRQEPGIATOLLASKGINFGWGSPSSRHAMYSKISQOTQPLSWLTLHFQHYHG	946
		: : : : : : : : : : : :	
Db	911	AYRTISGTETLLSHOETWTTDAFHARHGTVVVRGSMYAS-----LTSNIEVYG	959
		: : : : : : : : : : : : :	
RESULT 6			
US-09-620-412C-176			
; Sequence 176, Application US/09620412C			
; Patent No. 6448234			
; GENERAL INFORMATION:			
; APPLICANT: Steven P. Fling			
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND			
; TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION			
; FILE REFERENCE: 210121.469C7			
; CURRENT APPLICATION NUMBER: US/09/620.412C			
; CURRENT FILING DATE: 2000-07-20			
; NUMBER OF SEQ ID NOS: 363			
; SOFTWARE: FASTSEQ for Windows Version 3.0/4.0			
; SEQ ID NO 176			
; LENGTH: 982			
; TYPE: PRF			
; ORGANISM: Chlamydia			
; FEATURE:			
; NAME/KEY: VARIANT			
; LOCATION: (1)...(982)			

db 911 AYRTISGTETLLSHQETWTDAFHLARHGTVVRGSMYAS---LTSNIEVYG 9599

Query Match 12.7%; Score 647; DB 4; Length 982;
Best Local Similarity 25.4%; Pred. NO. 2e-46;
Matches 257; Conservative 156; Mismatches 388; Indels 212; Gaps 43;

Qy	39	SLGNKISLTGDTNHLNFCYLDNURYILAILQKTPNGBAAVTTIDYLSFFDTQKEGYIAK	98
Db	54	NLLGSFTLVGRHSLT---FENIR-----TSTNGAALS-----NSADGLF---	91
Qy	99	NLPESGGAIGYASPNSTVEIRDITGPIVFENNTCCRPFTSSNP--NAAV-----	147
Db	92	--TIEGFKELSFNCHNSLAVL-----PAATTNKGSTPTTITSTPSNGIYSKTDLLLLN	144
Qy	148	-----NKIR--EGGAIHAQNLVYINHNHDVGVFMKNFSYVRGGAISTANTFFVSENQSC	198
Db	145	NEKFSFYSNIVSGDGAIDAKSLTVQGISKLCVQENTAQADGGACQVVTFSFSAANEAP	204
Qy	199	FLFMDNICIOTNAG--KGGAIYA-----GTSNPF-----SNNCDLFTFNACCAG	243
Db	205	IAFVANV-----AGVRGGIAAVQDQGGQSVSSTEDPVVSFSRNTAVFDGNVAVRG	258
Qy	244	GAIFSPICSLTGNRGNIVFNN--RCFKN-----VETASSEASDGGAI	284
Db	259	GGIYS-----YGNVAFLNKGTITFLNNVASPVYIAAKQTPSQASNTSNNYGDGGA	310
Qy	285	KVITRLDVTGN-----RGRIFESDNITKNYGCAIYAPVVLVDNGPTTFINNIANN	335
Db	311	FCRNGAQAQSNNGSVSFDGEGVVFFSSNVAAGKGAIYAKKLUSVANCQPVQFLRIAND	370
Qy	336	KGAIYIDGTSNSKISADRHAIIFENI---VTNVTNAGTSTSANPPRRNAITVASS	391
Db	371	-GGAIYLGESGELSADYGDIIFDGNLKRKTAKENAAADVNGTVSS-----QAISMSGG	424
Qy	392	GEILLGAGSSONLIFYDPTIEVSN-----AGVSVSFKEADQTSVVFSGATVNSADPH	444
Db	425	KITTLRAGHQILFNDPEMANGNPOAQSSKLLKINDGEYTGDIVFAN---GSSTLY	481
Qy	445	QRNLQTKTAPLTLNSGFLCIEDHAQLTVNRRFTQGGVYSLNGAVLSCYKNGAGNS--	502
Db	482	QN-----VTIEGRIVLREKAKLSVNSLSOTGSLYMEAGSTLDFVTPQPQPPA	532
Qy	503	SNASITLKHGLNLSLSILKSGBAIPILLWEPYN--NSNNYTDATATFSLSDVKLS---	557
Db	533	ANOLITLSNLIHLSLSLLANNA---VTNPPTNPPAQDSHPAVIGST--TAGSVTISGP	587
Qy	558	IDYGNPSYESTD-----LTHALSSQPMLSITSEASDNOLSRDDMDFGLGNVPVHG	607
Db	588	FEDLDOTAYDRYDNLGSNQKINVLKQLGTKP--PANAPSDTL-----GNEMPXVG	637
Qy	608	WQGLTWGNAKTOPEPASSATITDPKANRFRHRTLLLTWLPAGYVPSPKHRSPLIANTPL	667
Db	638	YQGSWKLAW-----DPTANNGPYTLKATWTKTGYNPGPERSVASLVPNSL	682
Qy	668	WGNMLLATESLKNSAELTPSDHPFW-GITGGGLGMVYODPRENHHPGFHMRSSGYSAGMI	726
Db	683	WGS--ILDIRSAHAIGASVDGRSICGLWVSGVSNFFYHDDRALGOGYRYISGGYSLG---	739
Qy	727	AGQHTFSLKFSQTYTKLNERYAKNNV--SSKNYSQCEMLFSLQBGFLTLLKLVLGYSYG	784
Db	740	-ANSYFCGSSMFLAFTVEVFR-SKDYVVCRSNHHACIGSVYLSTQQA-----LCGSYLFG	792
Qy	785	DHNCHEFYTOG--ENLTSQGTFRSQT-----MGCAVFEDLPMKPFPGSTHILT--APPL	833
Db	793	DAFIRASYGRGNHMKTSTYFAESDVRWDDNCLAGEIGAGLPITVPSKLVNLNLRPEV	852
Qy	834	GALGIYSSLSHFTEVAGYAPRSFTKTPLINLVPIGVKGSFNMATORPOAWTVLAYQP	893
Db	853	QAEFYSADHESFTEEGDOARAFKS--GHLLNLSPVGVKFDRCST--HPNKYSFMAAYICD	910
Qy	894	LYROEPGIATOLLASKIWNFGSGPSRRHAMSXYKISQOQPLSWLTLHFQYHG	946

```

RESULT 7
US-09-556-877-190
; Sequence 190, Applicant
; Patent No. 6432916
; GENERAL INFORMATION:
;
; APPLICANT: Probst, H
; APPLICANT: Bhattacharya, S
; APPLICANT: Skeiky, Y
; APPLICANT: Fling, S
; APPLICANT: Maisonneuve, J
; TITLE OF INVENTION:
;
; FILE REFERENCE: 210
; CURRENT APPLICATION NUMBER:
; CURRENT FILING DATE:
; NUMBER OF SEQ ID NOS:
; SOFTWARE: FastSeq
; SEQ ID NO 190
; LENGTH: 1006
; TYPE: PRT
; ORGANISM: Chlamydia
US-09-556-877-190

```

Query Match	12.7%	Score 647;	DB 4;	Length 1006;
Best Local Similarity	25.4%	Pred. No. 2.1e-46;		
Matches 257;	Conservative 156;	Mismatches 388;	Indels 212;	Gaps 43;

Qy	39	SLSNKISLTGDTNHLNFCYLDNRLYALILQKTPNCGAAVTIDYLSFDTQKEGYFAK	98
Db	78	NLGGSFTVLGRGHSLT--FENIR-----TSTNGAALS-----NSAADGLF--	115
Qy	99	NLTPESGAGIYASPNSTVEIRDITGIPVIFENNTCCRPFTSNP--NAAV-----	147
Db	116	--TIEGFKELSFNCNSLAVL-----PAATTNKGQSOTPTTTTSPNGTIYSKTDLLLN	168
Qy	148	-----NKIR-EGGAHIAQNLXIHNHDVGFMKNFYSKVRGGAISTANTFVVSNQSC	198
Db	169	NEKFSFYSLNVSDDGGAIDAKSLTVQGISKLVCYQENTAQADGACQCVTFSFSAANEAP	228
Qy	199	FLPMDNICIQTNTAG-KGGAIYA-----GTSNSFE-----SNNCDLFFINNACCAG	243
Db	229	IAFVANY-----AGVRGGIAVQDQCQGVSSSTEDPVSFSRNTAVFEDGNVARVG	282
Qy	244	GAIFSPICSLTGNRGNTVFYNN--RCFKN-----VETASSEASDGGAI	284
Db	283	GGIYS-----YGNVAFNLNGKTLFLNNVASPVYIAAKQPTSGQASNTSNNYGDGAI	334
Qy	285	KVTTRLDVTGN-----RGRIFSDNITKYGGAIVAPVVLVDNGPTTFINNANN	335
Db	335	FCKNGAQAAGSNNGSVSFDGEGVYVTFSSNVAAGKGAIIYAKKLSVANCQVQVFLRIAND	394
Qy	336	KGGAIIYIDGTSNSKISADRHAIIFNENI-----VTNVTNANGTSTANPPRRNAITVASS	391
Db	395	-GGAIYIGESGEISLSADYGDIIFDGNLKTAKENAADVNGYTVSS-----QAISMCSG	448
Qy	392	GEILLGAGSSONLIFYDPIEVSN-----AGVSVSFNKEADOTGSVFSGATVNSADPH	444
Db	449	KITPLRAKAQHQLFNPNDIEMANGNNQPAOSSKLLKINDGEGYTGDIQIVAN---GSSTLY	505
Qy	445	QRNLQTKTAPPLTSLNCFIEBHAOLTVNRFQTQGVVSLNGCAVLSVCYKNAGNS--A	502
Db	506	QN-----VTIEQGRVIREKAKLSVNSLSQTGGSLYMEAGSTLDFVTFPPQPPPPA	556
Qy	503	SNASITLKHICLNLSSILKSAGETPLIWLVBPTN--NSNNYTDATAATFSLSDVKLS---	557
Db	557	ANQLITLNLHLSSLILLANNA---VTNPPTNPPAQDSDHPAIVGST-TAGSVTISGPFI	611
Qy	558	IDDYGNSPYESTD-----LTHALSSQPMLSITSEASDNLQRSDDDMDFFSGLNVPHYG	607
Db	612	FEDLDDTAYDRYDWLGNQSKINVLKQLQTKP--PANAPSDLTL-----GNEMPKYG	661

Qy	608	WQGLWTWGNAKTQDPEPASSATTTDPOKANRFHRTLLLTWLPAGYVSPKHRSPLIANTL	667
Dd	662	YQGSWKLAW-----DPNTANGPYTLTKATWTKTGYNGPGERVASLVPSNL	706
Qy	668	WGNMLLATESLKNSAELTPSDHPFW-GITCGGIGLMVVYQDPRENHPCGFHMRSRGYSAGMI	726
Dd	707	WGS-ILDIRSAHSIAQSVDGRSYCRLGWVSNNFFYHDROALGOGYRIYSGYSILG--	763
Qy	727	AGOTHTESLFQSOTYTKLNERYAKNNV--SSKNYSQCEMLFLSQBGEFLTTLKLVLGYSYG	784
Dd	764	-ANSYFGSSMEGLATEVFGR-SKDYVVCRRHHACIGSVYLSTQA-----LCGSYLFPG	816
Qy	785	DHNCHHYTGQ-ENLTSQGTFRQT-----MGAIVFDLPKMPFGSTHILT--APFL	833
Dd	817	DAFTIRASYGFGNQHMKTSYTFAEESDVWRDNCLAGEIGAGLPITVPISKLYLNEURPEV	876
Qy	834	GALGIYSSLHFTEVGAYPRSFSTKPTLINVLPIGVKGSEMNATORPOAWTVELAYQPV	893
Dd	877	QAEEFYADHESTFEEDQARAFKS-GHLLNLSYPVGVKKFDRCSST-HPNKYSFMAAYICD	934
Qy	894	LYRQEPGIATOLLASKGINFGSGPSRRHAMYSKIISOQTPLSWLTLHFQYHG	946
Dd	935	AYRTISGTETTLTSHOSTWTTDAFHARHGCVVYRGWSIAMS----LFSNTIEVIG	983

```

RESULT 8
US-09-620-412C-190
; Sequence 190, Application US/09620412C
; Patent No. 6448234
; GENERAL INFORMATION:
; APPLICANT: Steven P. Fling
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
; FILE REFERENCE: 210121.469C7
; CURRENT APPLICATION NUMBER: US/09/620.412C
; CURRENT FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 363
; SOFTWARE: FastSeq for Windows Version 3.0/4.0
; SEQ ID NO 190
; LENGTH: 1006
; TYPE: PRT
; ORGANISM: Chlamydia
US-09-620-412C-190

```

[illegible]

Qy	336	KGGAIIYDGTGNSKISADRHAIIENI----	VTVNTVANGTSTSANPPRRNAITVASSS	391
Db	395	GGAIYLGESGELSDYGDIIIPDGLKRTAKENAA	DVNGVTSS-----QAISMGSGG	448
Qy	392	GEILLAGSSONLIIFYDPIEVSN-----	AGVSYSFNKEADOTGSVVFSGATVNSADPH	444
Db	449	KITTLRAKAGHOIIFNDPIEMANGNNO	PAOSSKLLKINDGEGYTGDIIVFAN-----	GSSTLY 505
Qy	445	ORNLQTKTPALNLSNGFLCTIEDHAQULTVNR	FTGCGVSLGNAVLSCYKNGAGNS--A	502
Db	506	QN-----VTIEQGRIVLREKAKLSVNSLS	QSGSLYMEAGSTLDFVTPOPPQPPA	556
Qy	503	SNASITUKHIGLNUSSILKSGAETPLLWVEPTN	--NSNNYTADTAATFSLSDVKLS---L	557
Db	557	ANQILITNLNLSLSLANNNA-----	VTPNPPTPPAODSHPAVIGST-TAGSVY	TISGPFI 611
Qy	558	IDDXGNSPYESTD-----LTHALSSQPM	LSTISEASDNOLRSDMDDFSLGNVPHYG	607
Db	612	FEDLDDTAYDRYDWLGSGNQKINVLKQLGTRP	--PANAPSDLLT-----GNEMPKYG	661
Qy	608	WQGLWTWGWAKTQDPASSATITDPKANRFRH	RTLTLTLWLPAGYVPSPKHRSPLIANTL	667
Db	662	YOGSWKLAW-----DPNTANNGPYTLKAT	WTKTGTGPNGPVERVASLVPNSL	706
Qy	668	WGNMLLATESLKNSAELTPSDHPFW-GITCGG	GLMMVYQDPREHHGCFHWRSSGYSAGMI	726
Db	707	WGS-ILDIRSAHSIAQASDGRSYCGLWVSG	NFNFFYHDDRALGOGYRIISGGYSLG--	763
Qy	727	AGQTHFSLKFSQYTKLNERAKNNV--SSKNY	SCQEGMLFSLQGBFLLTKLVGLYSYG	784
Db	764	-ANSYFGSSMFLAFTVFG-RKDYVVC	RSHHACIGSVLSTQQA-----LCSYLFG	816
Qy	785	DHNCHEPYTOG-ENLITSQGTFRSQT-----	MGGAVFDDLPMKPFPGSTHILT--APFL	833
Db	817	DAFRASYGFCNQHKTSYTFABESDV	RWDNNCLAGEIGAGLPITVPSKLYLNELRPFV	876
Qy	834	GALGIYSSLSHFTVEVGAYPSRSTKTPLI	INVPIYIGVKSFMNATORQNAVTELAYQPV	893
Db	877	QAEFSAADHESFTFEGDQARAFKS-GHLL	NLSYFVGFKEDRCSST--HPNKYSFMAA	YICD 934
Qy	894	LYROEPGIATQLLASKGIWFGSGPS	SRSHAMYSKISQOTQPLSWLTLHFQYHG	946
Db	935	AYRTISCTFTLLSHQFTWTDAPHARHCV	VGVGWSWAS---TNSNFPVYG	983

```

RESULT 9
US-09-620-412C-321
; Sequence 321, Application US/09620412C
; Patent No. 6448234
; GENERAL INFORMATION:
; APPLICANT: Steven P. Fling
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
; FILE REFERENCE: 210121.469C7
; CURRENT APPLICATION NUMBER: US/09/620,412C
; CURRENT FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 363
; SOFTWARE: FastSeq for Windows Version 3.0/4.0
; SEQ ID NO 321
; LENGTH: 715
; TYPE: PRT
; ORGANISM: Chlamydia trachomatis
US-09-620-412C-321

```

	Query Match	11.9%;	Score 605.5;	DB 4;	Length 715;
	Best Local Similarity	27.2%;	Pred. No. 4.4e-43;		
	Matches 208;	Conservative 120;	Mismatches 277;	Indels 159;	Gaps
Qy	302	SDNITKNYGGAIYA-PV-----	-VTLDNGSTPYFIN-NIANKGGAIVDGTNS	348	
		: :	: : : :		
Db	11	SDNFQLSQGGGFPAIPGOAMATAGQTKPTLVHIGTAPFLGLGVVDVNDNGARVORVVG	S	70	
Ov	349	KISADRIAIFINENIVNTNVANGTSNPANPPRNNAITVASSSGEILLGAGSSONLIFYD	408		

Db 71 APAASLG--ISTGDVITAVDGA-----PINSATAMADALNG-----HH 106
QY 409 PIEVSNAGVSVNKEA--DOTGSVPSGATVNSADF-----HORNLOTKT-----452
Db 107 PGDV-----ISVTQWTKSGGRTGNVTL--AEGPPAEFCRYPSHWRLDIRTLGKHEHYI 160
QY 453 -PAPLTSLNGFLCTEDHAQUTVNR--FTQT-GGVVSLGNGAVLSCYKNGAGNSASNASIT 508
Db 161 KEAPTLKFTGLAEDDAELEINIFTQNTPTSLALGSGATLVGKHG-----KLN 212
QY 509 LKHIGLMSILKSGAIEPLLVEPTN--NSNNYTAOT--AATFSL-----DYKLSLIDD 560
Db 213 ITNLGVILPILILKEGSPPCIRVNPQDMTQNTGTGTPSPSTSSITPMIIFNGRLSIVDE 272
QY 561 YGNSPYESTDLTHALSOPMLISSEASDNOLRSD--DMDPFGSLNVPHYGWOGLWTGWA 617
Db 273 NYESVYDSMOLSRGKABQLLITETNDGQDLSNWOSLNTLSLPPHYGYQGLWTPNWI 332
QY 618 KT-----QDPEPASSATITDQKANR-----638
Db 333 TTYITLNNSSAPTSATSIAEQKKTSETFTPSNTTASIPNIKASGSGSASNSGE 392
QY 639 ---FHRLLTLWLPAGVVPSPKHSRPLIANTL---WGNMILLATESLKNASIELTPSDHPFW 692
Db 393 VTITKHTLVVWAPVGIVDPIRRGLDIANSVLVHSGRNMGLRSL-----PDNSWF 445
QY 693 GIYGGGLGMVYODPRENHGPHWRSSGYSAGMIA--GQHTFSLKFSQTYTKLNEYAK 750
Db 446 ALOGAATFTFKOORLSLHYGYSASKGYTVSSQAGAHGKFLLSFSQSDRMKEKETN 505
QY 751 NNYSSKNY---SCOGEMFLSLQGBFLTLKLVG--LYSYGDNCHHFVTOGENLTSQOTER 805
Db 506 NRLSSRYLSALCFEHPMFED-----RIALIGAAACNYGTHNRSFY--GTTKSSKGKFH 557
QY 806 SOTMGGAFFDL-----PMKPFGSTHILTAFLGALGIYSSLSHFTEVGAYPRSFSTKPL 861
Db 558 STTLGASLRCLELDSMPLR-----SIMLTPFAQALFSRTEPASIRESGLARLFTLRQAH 612
QY 862 INVLPVIGKGSFMNATORQOATVELAYQPVLYRQEPGATOLLASKGIWFGSGSPSSR 921
Db 613 TAVVSPIGIKGAYSSDTWPTLSWEMELAYQPTLYWKRPRLNTLLIQNNGSWVTNTPLAK 672
QY 922 HAMSYSKISQOTPLSWLTLHFQYHGFYSSSTFCNYLNGETALRF 965
Db 673 HSP-YGRGSHLSKFLKLFANTQAEVATSVSHYNAGGALVF 715

RESULT 10

US-09-556-877-175
; Sequence 175, Application US/09556877
; Patent No. 6432916
; GENERAL INFORMATION:
; APPLICANT: Probst, Peter
; APPLICANT: Bhatia, Ajay
; APPLICANT: Skeiky, Yasir
; APPLICANT: Fling, Steve
; APPLICANT: Maisonneuve, Jeff
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
; FILE REFERENCE: 210121.469C5
; CURRENT FILING DATE: 2000-04-19
; NUMBER OF SEQ ID NOS: 305
; SOFTWARE: FastSeq for Windows Version 3.0/4.0
; SEQ ID NO 175
; LENGTH: 880
; TYPE: PRP
; ORGANISM: Chlamydia
; FEATURE:
; LOCATION: (1)...(880)
; OTHER INFORMATION: Xaa = Any Amino Acid

US-09-556-877-175

Query Match 9.3%; Score 471.5; DB 4; Length 880;
Best Local Similarity 23.5%; Pred. NO. 1.9e-31;
Matches 231; Conservative 147; Mismatches 349; Indels 257; Gaps 46;
QY 29 PNSV-----PDPTKESL-----SNKISLTGDPHNLNCTNCLNLRILAILOKTPN 73
Db 40 PNHVVCTFFEDCTWESLFPALCAHASODDPLYVLGNSY----CWFYSKLHITDPKEALFK 95
QY 74 EGAAVITD--YLSFFD--TOKEGIVFAKNTLPESGGGAIGYASNPSPVEIRDIGPVIFE 130
Db 96 EKGDLSTQNERFLSFTDCSSKE-----SSPSI-IHQKNGQLSLR 133
QY 131 NN---TCCREFTSSNPNAVNKIREGAIHAQNLVINNHNDVVGEKMFNFSYVVGGAISTA 187
Db 134 NNGSMFCRHWAGS-----GGAISADAFSJOHNYLFTAENSCKGNGALQ-A 182
QY 188 NTFVSENOQCFLFMDNICIQNTAGKGAIYAGTSSSFESNCD-LFFINNACCAGAI 246
Db 183 QTFSLSRNVSPISFARN-----RADLNGAICC--SNLICSGNVNPLFTGNSATNGA- 234
QY 247 FSPICSLTGNRGNIVFYNNRCFNKVNETASSEADGGAIKVTTRLDVYTGNGRGRFFSDNIT 306
Db 235 ---IC-----CISDLNT-----SEKGSLSLACNOET-----LFASNSA 264
QY 307 KNYGGAIYAPVTVLDVNGPTYFFINNANNKGAIYIDGTSNKSISADRAHAIENENIVTN 366
Db 265 KEGGAIYAKHMLVRYNGPVSVFINNSA-KTGGAIATQSGGSLILAGEGVLFQ-----318
QY 367 VTNANGTSTANPPRRNAITVASSSGEILLGAGSSQ--LIFYDPTIEVSNAGYSVSFNKE 424
Db 319 ---NSORTSDQGLVRNAYILXK---DAILSSLEARNGDILFFDPI-----VQESSKE 365
QY 425 AD-----QTS-----SVVFSGATVNSADFQORNLOTKTPAPLTL 459
Db 366 SPLPSSLSQASVTSPTPATASPLVIQTSANRSVIFSSEERLSEEEKTPDNLTSQLQPIELK 425
QY 460 NGFLCTEDHAQLVNRFTQGVVSLGNGAVLSCYKNGAGNSASNASITLKHGLNLSII 519
Db 426 SGRVLKDRAVLSAPLSQDPOALLME-----AGTSLKTS-----DLKATL 469
QY 520 LKSGAEIPLWVEPTNNNNYTDATATF-----SLSDVKLSLIDDDYGNPSYESTDLTHA 574
Db 470 ---SIPL-----HSLDTEKSVTHAPNLSIQKIFLNSGDNFYNVEL---510
QY 575 LSSQ-----PMLSISEASDNOLRSDMDDFGSLNVPHYGWOGLWTGWAKTODPEPPASATI 630
Db 511 LSKEQNNIPLTLTPK-EQSHLHLPDGNLSS-----HFGYQGDWTFWKDSD-----556
QY 631 TDPQKANRFRHTLLTLWLPAGYVPSKHSRPLIANTLWGNM--LLATESLKNASIELTPSD 688
Db 557 -----GHSLIANWTPKNYVPHPERQSTLVANTLWNTYSDMQAVQSMINTT--AHGG 605
QY 689 HPFWGITGGGLGMVYODPRENH--CFHMRSSGYSAGMIAG--QHTFSLKFSQTYTKL 744
Db 606 AYLFGTWGSVAVSNLFFVYVHDSSGRPIDWNHHRSLGYLFGISTHSLDDHSLAAGQLLGKS 665
QY 745 NERY-AKNVYSSKNYSQCEMLFSLOEGFLTLKLVLGYLSYGDHNCHEFFYQGENLTSQ--801
Db 666 SDSFITSTETTSYIATVQAQLATSLMK-----ISQAACYNESIHELKTKYRSFSGEGF 718
QY 802 GTFRSOTMGAVFFDLPMPKPFGSTHILTAFLGALGIYSSLSHFTEVGAYP-----852
Db 719 GSWHSVAVSVEVCASIPVSNGS-----GLFSSFSIFSCLKQSGTQDGFEE 766
QY 853 ----RSEFTKTPLINVLPIGVKGSFMNATORQOATVEL-AYQPVLYRQEPGIATQLLA 907
Db 767 SGEIRSFSSASS-FRNISLPIGI--TFEKKSQKTRTYFFLQYIQLKRDVSGPVVLK 823
QY 908 SKGIWFGSGSPSSRHSAMYSKISQ 931
Db 824 NAVSWDAPMANLDSRAYMFLTNQ 847

RESULT 11

US-09-620-412C-175
; Sequence 175, Application US/09620412C
; Patent No. 6448234
; GENERAL INFORMATION:
; APPLICANT: Steven P. Fling
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
; FILE REFERENCE: 210121.469C7
; CURRENT APPLICATION NUMBER: US/09/620.412C
; CURRENT FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 363
; SOFTWARE: FastSeq for Windows Version 3.0/4.0
; SEQ ID NO 175
; LENGTH: 880
; TYPE: PR1
; ORGANISM: Chlamydia
; NAME/KEY: VARIANT
; LOCATION: (1)...(880)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-620-412C-175

Query Match 9.3%; Score 471.5; DB 4; Length 880;

Best Local Similarity 23.5%; Pred. No. 1.9e-31;

Matches 231; Conservative 147; Mismatches 349; Indels 257; Gaps 46;

QY 29 PNV-----PDPTKESL-----SNKISLTGDTNLTNLCYLDNRYLAILQKTPN 73
DB 40 PNHVCTFEEDCTMESLPALCAHASODPLYVLGNSY---CWFSKLHITDPKEALFK 95
QY 74 EGAATITD--YLSFFD--TQKEGYFAKNLTPESGALGYASPNSTVEIRDTIGPVIFE 130
DB 96 EKGDLISQNFRLSFTDCSKE-----SSPSI-IHQKNGQLSLR 133
QY 131 NN---TCRPTSTSPNPAVANKIREGGAIHAQNLYINHNDVVGFMKNFVYVGGAIATA 187
DB 134 NNGSMFCRNHAEGS-----GGAISADAFSLQHNLYLFTAFENSSKNGGAIQ-A 182
QY 188 NTFVVSQSCFLPMDNICIOTNTAGKGAIYAGTSNFSFNCD-LFFINNACCAGAI 246
DB 183 QTFSLRNSVPSIFARN-----RADLNGAICC--SNLICSGNVNPLFTGNSATNGGA- 234
QY 247 FSPICSLTGNRGNIYVNNRCFKNVETASSEASDGAIAKVTTRLDVTCNRRGRIFFSDNIT 306
DB 235 ---IC-----CISDLNT-----SEKGSLSLACNQT-----LFASNSA 264
QY 307 KNYGAIYAPVTVLDNGPTYFINNANKGAIYIDGTSNKSISADRHAIFNENIVTN 366
DB 265 KEKGAIYAKHMLRYNGPVFINNSA-KIGGAIQSGGSLILAGBSVLFQ-----318
QY 367 VTNANGTSTANPPRNATVASSSGEILLGAGSQN--LIFYDPIEVSNAGVSFNFKE 424
DB 319 ---NSQRTSDQGLVRNAILYKX---DAILSLSEARNGLIFFDPI-----VQESSKE 365
QY 425 AD-----QTG---SVVFSGATVNSADPHQNLQTKTAPLTL 459
DB 366 SPLPSSLOASVTSPTPATAPLVLQTSANRSVIFSSERLSEEEKTPDNLTSQLQOPIELK 425
QY 460 NGFLCIEDHAQLTNRFTQTGGVYSLGNAGVLSYCKNGAGNSASNASITLKHGLNLSI 519
DB 426 SGRVLKDRAVLSAPLSQDPOALLME-----AGTSLKTS-----DLKATL 469
QY 520 LKSGAEIPLLVETPNNSNNTADTAATF-----SLSDVKLSLIDDDYGNPSYESTDLTHA 574
DB 470 -----SIPL-----HSLDEKSVTIHAPNLSIQIFLSNCGDENFYENVEL---510
QY 575 LSSQ-----PMLSISEASDNLRSDDMFSGLVNPHYHGOGLWTGWAKTQDPEPASSATI 630
DB 511 LSKGONNIPLLTPK-BOSHLHLPDGNLSS-----HFGYQGDWTFWSKDSDE-----556

QY 631 TDPOKANRHRHTLLTLWLPAGVYVSPKHRSPLIANTLWGNM--LLATESLKNSAELTPSD 688
DB 557 -----GHSLIANTWPKNYVPHPERQSLVANTLWNTYSDMQAVOSMINT--AHGG 605
QY 689 HPFWGITGGGLGMVYQDPRENHP--GPHMRSSGYSGAGIAG--QTHFTSLKFSQTYTKL 744
DB 606 AYLFGTWSAVSNLFYVHDSSGKPIDNNHRSLSGLYLFGLGISTHSLDDHSFCLAAAGQLLGS 665
QY 745 NERY-AKNVSSKNYSCOGEMFLSLOEGFLITKLVLGLYSYGDHNCCHHFTYTOENLTSQ--801
DB 666 SDSFITSTETTSYATVQAQLATSLMK-----ISAQACYNESHELUKTKYRSFKEGF 718
QY 802 GTFRSOTMGAVFEDLPKMPFGSTHILTAFLGALGAYSSLSHFTFVGAYP-----852
DB 719 GSWHSVAVSGEVCASIPVSNGS-----GLSSFSISFKLQGFSGCTQDGFES 766
QY 853 ----RSFSTKTPLINVLVPIGVKGSFMNATORPQAWTVEL--AYQVLYRQBPQIATQLLA 907
DB 767 SGEIRSFSSASS-FRNLISLPIGT--TFEKKSQKTRTYVYFLGAYIQDLKRDVESGPVLLK 823
QY 908 SKGIWFGSGSPSSRHMSYKISQ 931
DB 824 NAVSMDAPMANLDSRAYMRLTNQ 847
RESULT 12
US-09-556-877-189
; Sequence 189, Application US/09556877
; Patent No. 6432916
; GENERAL INFORMATION:
; APPLICANT: Probst, Peter
; APPLICANT: Bhatia, Ajay
; APPLICANT: Steiky, Yasir
; APPLICANT: Fling, Steve
; APPLICANT: Maisonneuve, Jeff
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
; FILE REFERENCE: 210121.469C5
; CURRENT APPLICATION NUMBER: US/09/556.877
; CURRENT FILING DATE: 2000-04-19
; NUMBER OF SEQ ID NOS: 305
; SOFTWARE: FastSeq for Windows Version 3.0/4.0
; SEQ ID NO 189
; LENGTH: 866
; TYPE: PR1
; ORGANISM: Chlamydia
; NAME/KEY: VARIANT
; LOCATION: (1)...(866)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-556-877-189
Query Match 9.0%; Score 459.5; DB 4; Length 866;
Best Local Similarity 23.5%; Pred. No. 2e-30;
Matches 230; Conservative 146; Mismatches 355; Indels 249; Gaps 45;
QY 29 PNV-----PDPTKESL-----SNKISLTGDTNLTNLCYLDNRYLAILQKTPN 73
DB 26 PNHVVCTFEEDCTMESLPALCAHASODPLYVLGNSY---CWFSKLHITDPKEALFK 81
QY 74 EGAATITD--YLSFFD--TQKEGYFAKNLTPESGALGYASPNSTVEIRDTIGPVIFE 130
DB 82 EKGDLISQNFRLSFTDCSKE-----SSPSI-IHQKNGQLSLR 119
QY 131 NN---TCRPTSTSPNPAVANKIREGGAIHAQNLYINHNDVVGFMKNFVYVGGAIATA 187
DB 120 NNGSMFCRNHAEGS-----GGAISADAFSLQHNLYLFTAFENSSKNGGAIQ-A 168
QY 188 NTFVVSQSCFLPMDNICIOTNTAGKGAIYAGTSNFSFNCD-LFFINNACCAGAI 246
DB 169 QTFSLRNSVPSIFARN-----RADLNGAICC--SNLICSGNVNPLFTGNSATNGX- 220
QY 247 FSPICSLTGNRGNIYVNNRCFKNVETASSEASDGAIAKVTTRLDVTCNRRGRIFFSDNIT 306

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Db 221 ---IC-----CISDLNT-----SEKGS-----LSLACNQXTLFAS-NSA 250
Qy 307 KNYGAIYAPVTVLVDNGPTFYFINNIANNKGGAIYIDGTSNKSISADRHAIIENENIYTN 366
Db 251 KEGGAIYAKHMLVRYNGPVSFINNSA-KIGGAIYIQSGGSLSLAGEGSVLFON-----304
Qy 367 VTNANGTSTANPRRRAITVASSGEILLGAGSSON--LIFYDPIEVSNAAGVSFNFKE 424
Db 305 ---NSQRTSDOGLVRNAIYLEK---DAILSSLEARNGDILFFDPI-----VOESSSKE 351
Qy 425 AD-----QTG---SVFSGATVNSADPHQRNLQTKTPAPITLS 459
Db 352 SPLPSSLOASVTSPTPATASPLVIQTSANRVSIFSSERLSEETPDNLTSLQLOQPIELK 411
Qy 460 NGFLCIEDHAOLTVNRRFTQGTGVVSLGNGAVLSCYKNGAGNSASNASITLKHIGLNLSSI 519
Db 412 SGRVLKDRVLSXPSLSDQPALLIME-----AGTS-----443
Qy 520 LKSGAEIPLLWVE-PTNNSNNYTADTAATFSLSDVKLSLIDDYGNPSYESTDLTHALSSQ 578
Db 444 LKTSXDLKLTXTSPLHSLDTEKSVTHAPNLSIQKIFLSNGDENFYENVEL---LSKE 500
Qy 579 ---PMLSISASDNQLRSDMDPFGSLNVPHYGQGLTWGAKTQDPEPASTATIDPQ 634
Db 501 QNNIPLTLTPK-EQSHLHLPDGNLSS---HFGYQGDWTFSWKDSDE-----542
Qy 635 KANRFRHTLLTLTPAGVVPSPKHSRPLIANTLAGNM--LLATESLKNASAEITPSDHPFW 692
Db 543 -----GHSLIANWTPKNYVPHPERQSTLVANTLWNTYSDMQAVOSMINTT--AHGGAYLF 595
Qy 693 GITGGGLMMVYQDPRENHP--GFHMRSSGYSAGMIAG--QTHFTSLKFSQTYTKLNERY 748
Db 596 GTWGSAYNLVYVHDSSCKPIDNHNHRSGLVYFGISTHSLDDHSECLAAAGLLCKSSDSF 655
Qy 749 -AKNNVSKNYSKOGEMFLFSLOEGLTLTKLVGLYSYGDHNCCHFYTOGENLTQ--GTFR 805
Db 656 ITSTETTSYIATVQAQLATSLMK-----ISAQACYNESITHELTKYRSFSGEFGSWH 708
Qy 806 SQTWGGAVFFDLPMPKPGFSTHILTAFLGALGIYSSLSHFTFVGAYP-----852
Db 709 SVAVSVEGCASIPVSNGS-----GLFSSFSIFSKLOGFSGTQDGFEESSGEI 756
Qy 853 RSFSTKTPLINLVPIGVKGSFMNATORPOAWTVEL-AYQPVLYRQEPGIATQLLASKGI 911
Db 757 RSFSASS-FRNLSPIGI--TFEKKSKQTRYYYFLGAYIODLKRDESGPVLLKNAVS 813
Qy 912 WFGSGSPSSRHAMSKYSQ 931
Db 814 WDAPMANLDSRAYMFRLTNQ 833
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RESULT 13

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US-09-620-412C-189
; Sequence 189, Application US/09G20412C
; Patent No. 6448234
; GENERAL INFORMATION:
; APPLICANT: Steven P. Fling
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
; FILE REFERENCE: 210121.469C7
; CURRENT FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 363
; SOFTWARE: FastSeq for Windows Version 3.0/4.0
; SEQ ID NO 189
; LENGTH: 866
; TYPE: PRT
; ORGANISM: Chlamydia
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(866)
; OTHER INFORMATION: Xaa = Any Amino Acid
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US-09-620-412C-189
Query Match 9.0% Score 459.5; DB 4; Length 866;
Best Local Similarity 23.5%; Pred. No. 2e-30;
Matches 230; Conservative 146; Mismatches 355; Indels 249; Gaps 45;
Qy 29 PNSV-----PDPTKRESL-----SNKISLTGDTHTNLTCYLDNLRYTLAILQKTPN 73
Db 26 PNHVVCFFEDCTWESLFPALCAHASODDPLYVLGNSY---CWFVSKLHITDKPEALFK 81
Qy 74 EGAAVTITD--YLSFFD--TQKEGIYFAKNLTPESSGGAIGYASPNSTVEIIRDTTGPVIFE 130
Db 82 EKGDLISQNFRLFTDCSSK-----SSPSI-IHQKNGQLSLR 119
Qy 131 NN---TCRPTTSSNPAAVNKIREGGAITHAQNLYINNHHDVVGMKFNFSVVRGALSTA 187
Db 120 NNGSMFCRNIAEGS-----GGAISADAFSLQHNLYLFTAFEESSNGGGAIQ-A 168
Qy 188 NTFVVENSCFLFMDNICIQTNTAGKGAIYAGTSNFSFNCCD-LFFINNACCAGAI 246
Db 169 QTFSLSRNVSPISFARN-----RADLNGAICC--SNLICSGNVNPLFTGNSATNGGX- 220
Qy 247 FSPICSLTGNRGNIYFNNRCFKVETASSEASDGGAIKVTTRLDVTGNRGRIFSDNIT 306
Db 221 ---IC-----CISDLNT-----SEKGS-----LSLACNQXTLFAS-NSA 250
Qy 307 KNYGAIYAPVTVLVDNGPTFYFINNIANNKGGAIYIDGTSNKSISADRHAIIENENIYTN 366
Db 251 KEGGAIYAKHMLVRYNGPVSFINNSA-KIGGAIYIQSGGSLSLAGEGSVLFON-----304
Qy 367 VTNANGTSTANPRRRAITVASSGEILLGAGSSON--LIFYDPIEVSNAAGVSFNFKE 424
Db 305 ---NSQRTSDOGLVRNAIYLEK---DAILSSLEARNGDILFFDPI-----VOESSSKE 351
Qy 425 AD-----QTG---SVFSGATVNSADPHQRNLQTKTPAPITLS 459
Db 352 SPLPSSLOASVTSPTPATASPLVIQTSANRVSIFSSERLSEETPDNLTSLQLOQPIELK 411
Qy 460 NGFLCIEDHAOLTVNRRFTQGTGVVSLGNGAVLSCYKNGAGNSASNASITLKHIGLNLSSI 519
Db 412 SGRVLKDRVLSXPSLSDQPALLIME-----AGTS-----443
Qy 520 LKSGAEIPLLWVE-PTNNSNNYTADTAATFSLSDVKLSLIDDYGNPSYESTDLTHALSSQ 578
Db 444 LKTSXDLKLTXTSPLHSLDTEKSVTHAPNLSIQKIFLSNGDENFYENVEL---LSKE 500
Qy 579 ---PMLSISASDNQLRSDMDPFGSLNVPHYGQGLTWGAKTQDPEPASTATIDPQ 634
Db 501 QNNIPLTLTPK-EQSHLHLPDGNLSS---HFGYQGDWTFSWKDSDE-----542
Qy 635 KANRFRHTLLTLTPAGVVPSPKHSRPLIANTLAGNM--LLATESLKNASAEITPSDHPFW 692
Db 543 -----GHSLIANWTPKNYVPHPERQSTLVANTLWNTYSDMQAVOSMINTT--AHGGAYLF 595
Qy 693 GITGGGLMMVYQDPRENHP--GFHMRSSGYSAGMIAG--QTHFTSLKFSQTYTKLNERY 748
Db 596 GTWGSAYNLVYVHDSSCKPIDNHNHRSGLVYFGISTHSLDDHSECLAAAGLLCKSSDSF 655
Qy 749 -AKNNVSKNYSKOGEMFLFSLOEGLTLTKLVGLYSYGDHNCCHFYTOGENLTQ--GTFR 805
Db 656 ITSTETTSYIATVQAQLATSLMK-----ISAQACYNESITHELTKYRSFSGEFGSWH 708
Qy 806 SQTWGGAVFFDLPMPKPGFSTHILTAFLGALGIYSSLSHFTFVGAYP-----852
Db 709 SVAVSVEGCASIPVSNGS-----GLFSSFSIFSKLOGFSGTQDGFEESSGEI 756
Qy 853 RSFSTKTPLINLVPIGVKGSFMNATORPOAWTVEL-AYQPVLYRQEPGIATQLLASKGI 911
Db 757 RSFSASS-FRNLSPIGI--TFEKKSKQTRYYYFLGAYIODLKRDESGPVLLKNAVS 813
Qy 912 WFGSGSPSSRHAMSKYSQ 931
Db 814 WDAPMANLDSRAYMFRLTNQ 833
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RESULT 14
US-09-556-877-180
; Sequence 180, Application US/09556877
; Patent No. 6432916
; GENERAL INFORMATION:
; APPLICANT: Probst, Peter
; APPLICANT: Bhatia, Ajay
; APPLICANT: Skeiky, Yasir
; APPLICANT: Fling, Steve
; APPLICANT: Maisonneuve, Jeff
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
; FILE REFERENCE: 210121.469C5
; CURRENT APPLICATION NUMBER: US/09/556,877
; CURRENT FILING DATE: 2000-04-19
; NUMBER OF SEQ ID NOS: 305
; SOFTWARE: FastSeq for Windows Version 3.0/4.0
; SEQ ID NO 180
; LENGTH: 1752
; TYPE: PRT
; ORGANISM: Chlamydia
US-09-556-877-180

Query Match 7.8%; Score 398.5; DB 4; Length 1752;
Best Local Similarity 23.8%; Pred. No. 1.1e-24;
Matches 271; Conservative 135; Mismatches 379; Indels 353; Gaps 60;

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Db 701 LIDIV--VDTT-----ISKN-TAKKGGI-YAKKAKMSRIDOLNISENSAT-----EIG- 745

QY 127 VIFENNTCPRPTSSNPNAV-----NKI-REGGAIHAQNLYINHNHVDVGFMKN-----175
Db 746 ----GGICCK--ESLELDALVSLVTENLVKGGGLHAKTVNISNLKSGFSSNNKANS 799

QY 176 -----PSYVRGAI-----STANTFVVS 193
Db 800 SSTGVATTASAPAAAAAASLQAAAAAPSPATPTYSVGVGAIYGEKVTFSQCSGTCQFS 859

QY 194 ENQSCFLFMDNICIQNTAGKGAIVAGTYSNFSNCDLFFI-----NNACC 241
Db 860 GNOA-----IDNPSQSSSLNVGGAIAKTSLSIGSDAGTSYIFSGNSYSTGKSQTGQI 915

QY 242 AGGAIFSPICSLTNGRGNIVFYNNRC-FKNVETASSEASDGAIKVT-----TFLDVT 293
Db 916 AGGAIYSPVTL---NCPATFSNNTASTATPTSTSSDGSNGSIKDTGGAIAGTAITUS 972

QY 294 G-----NRGRIFFSDNITKNYGGAI 313
Db 973 GVSFSGNTADLGAALGTLANANTPSATSGSQNSITEKITLNGSFIFERN-QANKRGAI 1031

QY 314 YAPVTLVDNGTYTFNNIANKKGAIYI-DGTSNKSISADRHAIIFENIVTNTNAN 371
Db 1032 YSPSVSIKGNNTI-FNQNTSTHDGSAIYFTKDATIESLGS-----VLEFGNNVT-ATQAS 1084

QY 372 GTSTANPPRRN-----AITVASSSGEILLGAGSSON-----403
Db 1085 SATSQNTNTANYGAIFGDPGCTTOSQTDAILTLASSGNITFFNSLQNNQGGDTPASK 1144

QY 404 -----LIFYDPIEVS-----NAGVSVPNKEDQ-----TGSVVF 433
Db 1145 PCSIAGYKVLSQLAAKGTISFFDCVHTSTKKTGTQNVYETLDINKENSNPYTGTVF 1204

QY 434 SGATVNSADFHORNLOTKTPAPLTLSNGFLCIEDHAQLTVNRFTQ-TGGVVSLNGAVUS 492
Db 1205 -----SSELHEN--KSYIPQNAIHLNGTIVLKERKTELHVVSFEQEGSKLIMEPCAVLS 1256
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Db 860 GNOA-----IDNNPSQSLNWQGGAIYAKTSLSIGSSDAGTSYIFSGNSYSTGKSQTTGOI 915
QY 242 AGGAIFSPICSLTGRGNIVFYNNRC-FKNVETASSEASDGGAIKVT-----TRLDVT 293
Db 916 AGGAIYSPVTTL---NCPATFSNNTASIAIATPKTSSDGGSGNSIKDTIGGAIAGTAITLS 972
QY 294 G-----NCRGRIFFSDNITKNYGGAI 313
Db 973 GYSRFSGNTADLGAALGTLANANTPSATSGSONSITEKITLENGSFIFERN-QANKRGAI 1031
QY 314 YAPVTVLDNGPTYFINNTANNKGAIYI--DCTSNSKISADRHAIFNENIVTNVTNAN 371
Db 1032 YSPSVSIKGNIT-FQNTSTHDGSAIYFTKDATIESLGS-----VLEFGNNVT-ATQAS 1084
QY 372 GTSTSANPPRRN-----AITVASSSGEILLGAGSSQN----- 403
Db 1085 SATSGONTNTANYGAIFGDPQTQOSSQTDAILTLASSGNITFSNNSLQNNQGDTPASK 1144
QY 404 -----LIFYDPIEVS-----NAGVSVFPNKADQ---TGSVVF 433
Db 1145 FCSIAGYVKLSLOAKGKTIISFFDCVHTSTKKTGSTQNYVETLIDINKEENSNPYGTIIVF 1204
QY 434 SGATVNSADFHQNLQTKTPAPLTLSNGFLCIEDHAQLTVNRFQ-TGGVWSLGGAVLS 492
Db 1205 -----SSELHEN--KSYIPQNAIHLNGTFLVKTELHVSVFEQKESKLIMEPGAVLS 1256
QY 493 CYKNGAGNSASASTLKHIGLNLSSI-LKSGAEI---PLLWVEPTNNSNN----- 539
Db 1257 -----NQNIANGALAINGLTLDLSMGTPOAGEIFSPPELRIVATTSASGGSGVSSSI 1310
QY 540 -----YTADTAATFSLSDVK-----LSLIDDYGN---SPYESTDLTHALSSOP 579
Db 1311 PTNPKRISAAVPSGSAATPTMSENKVF LTGDLTLDPNNGFYQNPMLGSDLDVPLIKLP 1370
QY 580 MLSISEASDNQLRSDMDPFSGLNVPHYGQGLWTGWAKTQDPEPASSATITDPQKANRF 639
Db 1371 -----TNTSDVQVY--DLTSLGDLFPQKGYMGWTILD-----SNPQTGKIQ 1409
QY 640 HFTLLLTWLPAGYVPSPKHRSPLIANTLWG---NMLLATESL---KNSAELTP-SDHPF 691
Db 1410 ARWTFDTRYRWYIIPRDNH---FYANSILGSONSMIVVKQGLNNMLNNAREDDIAYNNF 1466
QY 692 WGITGGGLGMVYQDPRENHFGFHRKSSGYSAGMIAGQHTFSL--KFSQTYTKLNERYA 749
Db 1467 W---VSGVGTFLAQOQTPLSEEFYSYRGTSVAIDAKPQDFILGNAFSKIIVGKTKAIKK 1523
QY 750 KNNVSK--NYSCQ-----GEMFLSL---QEGFLTLKLV-GLYSYGDHNCCHFYTQGENL 798
Db 1524 MHNYPHKGSEYSYQASVYGGKFLYELLNKHQHWALPFLIQGVVSYG-HIKHDTTTLYPSI 1582
QY 799 TSOGTFRSQTMGG---AVFFDLPKMPGSGTHILTAFLGALGIYSSL--SHFTEVGAYP 852
Db 1583 HERNKGDWDLGLWDLADLRISMDLKEPSSDKSRKITV--YGELE-YSSIRKQKQFTEIDYDP 1639
QY 853 RSFSTKRTPLINVLVPTIG--VKGSFNMNATORPOAWTVELAYQPVLYROEPGIATOLIAS 908
Db 1640 RHFD-DCAYRNLSLPVGCAGEAIMNCNILMYN-KLALAYMPSIYRNNPVCYRVLSS 1695
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Search completed: February 4, 2003, 20:59:48
Job time : 46 secs



GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 4, 2003, 19:08:07 ; Search time 84 seconds
(without alignments)
1530.796 Million cell updates/sec

Title: US-09-677-752-2

Perfect score: 5086

Sequence: 1 MKKAPFFFLIGNSLGLARE.....GFSSSTFCNYLNGEIALRF 965

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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 - 2: /SID22/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
 - 3: /SID22/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5086	100.0	965	AAE23453	Chlamydia trachoma
2	5047	99.2	989	AAI37242	Chlamydia trachoma
3	4994.5	98.2	964	AAI13634	C. trachomatis pmp
4	4994.5	98.2	964	AAI83202	Protein encoded by
5	4994.5	98.2	964	AAI94173	Chlamydia protein
6	4919.5	96.7	977	AAI13640	C. trachomatis pmp
7	4919.5	96.7	977	AAI83208	Protein encoded by
8	4919.5	96.7	977	AAI94179	Chlamydia protein
9	4884	96.0	956	AAE23486	Chlamydia trachoma
10	2605	51.2	500	AAE23472	Chlamydia trachoma

11	1123.5	22.1	931	21	AAI92833	C. pneumoniae CPN1
12	1120.5	22.0	938	23	ABN90528	Chlamydia pneumoniae
13	1120.5	22.0	940	20	AAI35082	Chlamydia pneumoniae
14	1057.5	20.8	969	20	AAI35083	Chlamydia pneumoniae
15	1057.5	20.8	1000	21	AAI92832	C. pneumoniae CPN1
16	1052	20.7	934	23	ABN90529	Chlamydia pneumoniae
17	989.5	19.5	963	21	AAI95551	C. pneumoniae CPN1
18	947.5	18.6	954	21	AAI92830	C. pneumoniae CPN1
19	915	18.0	788	21	AAI92831	C. pneumoniae CPN1
20	727	14.3	822	20	AAI35088	Chlamydia pneumoniae
21	651.5	12.8	1013	20	AAI16738	C. trachomatis F s
22	649.5	12.8	918	21	AAI69369	Amino acid sequenc
23	647	12.7	982	21	AAI13633	C. trachomatis pmp
24	647	12.7	982	22	AAI83201	Protein encoded by
25	647	12.7	982	23	ABN94172	Chlamydia protein
26	647	12.7	1006	21	AAI13639	C. trachomatis pmp
27	647	12.7	1006	22	AAI83207	Protein encoded by
28	647	12.7	1006	23	ABN94178	Chlamydia protein
29	646.5	12.7	1013	20	AAI16737	C. trachomatis B s
30	645	12.7	925	21	AAI99843	Chlamydia pneumoniae
31	645	12.7	936	21	AAI99842	Chlamydia pneumoniae
32	645	12.7	936	23	ABN90602	Chlamydia pneumoniae
33	642	12.6	1012	20	AAI16735	C. trachomatis LGV
34	637.5	12.5	918	20	AAI88422	Chlamydia pneumoniae
35	636	12.5	926	23	ABN88228	Chlamydia polypt
36	620	12.2	930	20	AAI35052	Chlamydia pneumoniae
37	617	12.1	930	23	ABN90548	Chlamydia pneumoniae
38	615	12.1	930	21	AAI90240	Chlamydia antigen
39	608	12.0	930	20	AAI88424	Chlamydia pneumoniae
40	605.5	11.9	715	22	AAI83273	Chlamydia trachoma
41	605.5	11.9	715	23	ABN94244	Chlamydia trachoma
42	597	11.7	928	20	AAI88417	Chlamydia pneumoniae
43	597	11.7	928	21	AAI90236	Chlamydia antigen
44	597	11.7	928	23	ABN90583	Chlamydia pneumoniae
45	597	11.7	949	20	AAI35060	Chlamydia pneumoniae

ALIGNMENTS

RESULT 1	
AAE23453	
ID	AAE23453 standard; Protein; 965 AA.
XX	
AC	AAE23453;
XX	
DT	27-AUG-2002 (first entry)
XX	
DE	Chlamydia trachomatis L2 PMPE protein #1.
XX	
KW	Polymorphic membrane protein; PMPE; vaccine; trachoma; PID; LGV;
KW	urethritis; epididymitis; conjunctivitis; cervicitis; cervical cancer;
KW	pelvic inflammatory disease; lymphogranuloma venereum; tubal occlusion;
KW	endometritis; salpingitis; inflammatory heart disease; cardiomyopathy;
KW	infertility; autoimmune myocarditis; atherosclerosis; infection;
XX	arthritis.
OS	Chlamydia trachomatis.
XX	
PN	WO200228998-A2.
XX	
PD	11-APR-2002.
XX	
PF	28-SEP-2001; 2001WO-US30345.
XX	
PR	02-OCT-2000; 2000US-0677752.
XX	
PA	(ANTE-) ANTEX BIOLOGICS INC.
XX	
PI	Jackson WJ;
XX	
DR	WPI; 2002-426107/45.
DR	N-PSDB; AAD37798.

XX Novel purified Chlamydia polymorphic membrane protein E or I, useful
PT for preparing vaccines for preventing or treating diseases associated
PT with Chlamydia infection such as trachoma, and infertility -
XX
XX Claim 1; Fig 5; 160pp; English.
XX
XX The invention relates to Chlamydia sp. polymorphic membrane protein
CC (PMP) E and PMPE and nucleic acid molecules encoding such proteins.
CC PMPE and PMPE polypeptides, nucleic acids and vaccines are useful for
CC preventing, treating or ameliorating trachoma, conjunctivitis, tubal
CC occlusion, cervicitis, cervical cancer, pelvic inflammatory disease
CC (PID), lymphogranuloma venereum (LGV), endometritis, epididymitis,
CC salpingitis, infertility, reactive arthritis, inflammatory heart
CC disease, urethritis, autoimmune myocarditis, cardiomyopathy and
CC atherosclerosis. They are also useful as reagents for clinical or
CC medical diagnosis of Chlamydia infections. The present sequence is
CC Chlamydia trachomatis L2 PMPE protein.
XX
SQ Sequence 965 AA;

Query Match 100.0%; Score 5086; DB 23; Length 965;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 965; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKKAFFFFLIGNSLGLAREVPSRIFLMPNSVPDPTKESLNKISLTGDTNLTNCLYLDN 60
DB 1 MKKAFFFFLIGNSLGLAREVPSRIFLMPNSVPDPTKESLNKISLTGDTNLTNCLYLDN 60

QY 61 LRYILAILQKTPNEGAATITDYLSEFFDTQKEGIYFAKNLTPESGGAIGYASPNSTVEI 120
DB 61 LRYILAILQKTPNEGAATITDYLSEFFDTQKEGIYFAKNLTPESGGAIGYASPNSTVEI 120

QY 121 RDTIGPVIFENNTCCRPFTSSNPNAVNKIREGGAIHAQNLVYINNHVDVGFKNFVSVR 180
DB 121 RDTIGPVIFENNTCCRPFTSSNPNAVNKIREGGAIHAQNLVYINNHVDVGFKNFVSVR 180

QY 181 GGAISTANTFVSENSQSCFLFMDNICIQTNTAGKGGAIYAGTNSFESNCCDLFFINNAC 240
DB 181 GGAISTANTFVSENSQSCFLFMDNICIQTNTAGKGGAIYAGTNSFESNCCDLFFINNAC 240

QY 241 CAGGAIFSPICSLTGNRGNIVFYNNRCFKNVETASSEASDGGAIKVTRLDVTGNRGRIF 300
DB 241 CAGGAIFSPICSLTGNRGNIVFYNNRCFKNVETASSEASDGGAIKVTRLDVTGNRGRIF 300

QY 301 FSDNITKNGGAIYAPVVTLYDNGPTYFNNIANNKGGAIYIDGTSNKSISADRHAIIFN 360
DB 301 FSDNITKNGGAIYAPVVTLYDNGPTYFNNIANNKGGAIYIDGTSNKSISADRHAIIFN 360

QY 361 ENIVTNVNTANGTSTANPPRRNAITVASSSGEILLGAGSSQNLIFYDPIEVSNAGSVS 420
DB 361 ENIVTNVNTANGTSTANPPRRNAITVASSSGEILLGAGSSQNLIFYDPIEVSNAGSVS 420

QY 421 FNKEADQTVGVFSGATVNSADFHORNIQTTPAPLTLSNGFLCTIEDHAQLTVNRFTQTG 480
DB 421 FNKEADQTVGVFSGATVNSADFHORNIQTTPAPLTLSNGFLCTIEDHAQLTVNRFTQTG 480

QY 481 GVSIGNGAVLSCKYNGAGNSASASITLKHIGLNSILKSGAEIPLLWVEPTNNSNNY 540
DB 481 GVSIGNGAVLSCKYNGAGNSASASITLKHIGLNSILKSGAEIPLLWVEPTNNSNNY 540

QY 541 TADTAATFSLSDVKLSLIDDDYGNPSYESTDLTHALSSQPMLSISEASDQLRSDMDPSG 600
DB 541 TADTAATFSLSDVKLSLIDDDYGNPSYESTDLTHALSSQPMLSISEASDQLRSDMDPSG 600

QY 601 LNVPHYHQGLWTGWAKTQDEPASSATITDPOKANFRHRTLLTLTWLPAGYVSPKHS 660
DB 601 LNVPHYHQGLWTGWAKTQDEPASSATITDPOKANFRHRTLLTLTWLPAGYVSPKHS 660

QY 661 PLIANTLWGNMLLATESLKNASAEITPSDHPFWGLTGGGLGMVYODPRENHPGFHMRSSG 720
DB 661 PLIANTLWGNMLLATESLKNASAEITPSDHPFWGLTGGGLGMVYODPRENHPGFHMRSSG 720

QY 721 YSAGMIAGQTHFTSLKFSQTYTKLNERYAKNNVSKNYSCQGMFLSLQEGFLTKLVGL 780
DB 721 YSAGMIAGQTHFTSLKFSQTYTKLNERYAKNNVSKNYSCQGMFLSLQEGFLTKLVGL 780

QY 781 YSYGDHNCHEFTYQGENLTSGTFRSQTMGGAVFDDLPKPKFGSTHILTAPFLGALGIYS 840
DB 781 YSYGDHNCHEFTYQGENLTSGTFRSQTMGGAVFDDLPKPKFGSTHILTAPFLGALGIYS 840

QY 841 SLSHTEVGAYPRSFSTKTPLINLVPIGVKGSFNATQPOAWTVELAYQPVLYRQEPG 900
DB 841 SLSHTEVGAYPRSFSTKTPLINLVPIGVKGSFNATQPOAWTVELAYQPVLYRQEPG 900

QY 901 IATQLLASKGIWFGSGSPSSRRHMSYKISQQTQPLSLWTLHFQYHGFYSSSTFCNYLNCE 960
DB 901 IATQLLASKGIWFGSGSPSSRRHMSYKISQQTQPLSLWTLHFQYHGFYSSSTFCNYLNCE 960

QY 961 IALRF 965
DB 961 IALRF 965

RESULT 2
AAI37242
ID AAY37242 standard; Protein; 989 AA.
XX AC AAY37242;
XX AC
DT 07-OCT-1999 (first entry)
XX
DE Chlamydia trachomatis cellular envelope protein.
XX
KW Vaccine; eye disease; conventional trachoma; nonendemic trachoma;
KW paratrachoma; inclusion conjunctivitis; genital disease; perihhepatitis;
KW nongonococcal urethritis; epididymitis; cervicitis; salpingitis;
KW bartholinitis; pneumopathy; venereal lymphogranulomatosis.
XX
OS Chlamydia trachomatis.
XX
PN W09928475-A2.
XX
PD 10-JUN-1999.
XX
PF 27-NOV-1998; 98WO-IB01939.
XX
PR 04-NOV-1998; 98US-0107077.
PR 28-NOV-1997; 97FR-0015041.
PR 17-DEC-1997; 97FR-0016034.
XX
PA (GEST) GENSET.
XX
PI Griffiths R;
XX
DR WPI; 1999-371125/31.
XX
PT Genome sequence of Chlamydia trachomatis
XX
PS Disclosure; Page 999-1000; 1755pp; English.
XX
CC AAY36754-Y37949 are encoded by open reading frames (ORFs) of the genome
CC of Chlamydia trachomatis (see AA201425). The polypeptides can be used as
CC vaccines against Chlamydia trachomatis. Antisense and ribozyme sequences
CC can also be used to control growth of the microorganism. Chlamydia
CC trachomatis is responsible for a large number of diseases, e.g. eye
CC diseases such as conventional trachoma, nonendemic trachoma,
CC paratrachoma, and inclusion conjunctivitis; genital diseases such as
CC nongonococcal urethritis, epididymitis, cervicitis, salpingitis,
CC perihhepatitis, bartholinitis; pneumopathy in breast feeding infants;
CC and venereal lymphogranulomatosis. The polypeptides of the invention
CC may be of use in treating these diseases.
XX
SQ Sequence 989 AA;

Query Match

99.2%; Score 5047; DB 20; Length 989;

Best Local Similarity 99.3%; Pred. No. 0;
Matches 958; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 MKKAFFFLIGNSLGLAREVPSRIFLMPNSVDPPTKESLSNKISLGLDTHNLTCYLDN 60
DB 25 MKKAFFFLIGSSUGLAREVPSRIFLMPNSVDPPTKESLSNKISLGLDTHNLTCYLDN 84
QY 61 LRYLAILQKTPNEGAATITDYLSPFDQKEGIYFAKNLTPESGGAIGYASPNPVEI 120
DB 85 LRYLAILQKTPNEGAATITDYLSPFDQKEGIYFAKNLTPESGGAIGYASPNPVEI 144
QY 121 RDTIGPVIFENNTCCRPFTSSNPNAAVNKIREGAIHAQNLYINHNHVVGVGFMKFSYVR 180
DB 145 RDTIGPVIFENNTCCRPFTSSNPNAAVNKIREGAIHAQNLYINHNHVVGVGFMKFSYVR 204
QY 181 GGAISTANTFVWSNQCFLFMDNICIQTNTAGKGGAIYAGTSNFSFNCDLFFINNAC 240
DB 205 GGAISTANTFVWSNQCFLFMDNICIQTNTAGKGGAIYAGTSNFSFNCDLFFINNAC 264
QY 241 CAGGAIFSPICSLTGNRGNIYFVNNRCFKNVTASSEASDGAIKVTRLDVTGNRGRIF 300
DB 265 CAGGAIFSPICSLTGNRGNIYFVNNRCFKNVTASSEASDGAIKVTRLDVTGNRGRIF 324
QY 301 FSDNITKNYGGAIYAPVVTLDVNGPTYFINNIANNKGGAIYIDGTSNKSISADRHAIIFN 360
DB 325 FSDNITKNYGGAIYAPVVTLDVNGPTYFINNIANNKGGAIYIDGTSNKSISADRHAIIFN 384
QY 361 ENIVNTVNTANGSTSANPRRRAITVASSSGEITLLGAGSSONLIFYDPIEVSNAGYSVS 420
DB 385 ENIVNTVNTANGSTSANPRRRAITVASSSGEITLLGAGSSONLIFYDPIEVSNAGYSVS 444
QY 421 FNKEADQGSVFGATVNSADFHQNLQTKTAPLTLNSGFLCIEDHQAOLTVNRFTQTG 480
DB 445 FNKEADQGSVFGATVNSADFHQNLQTKTAPLTLNSGFLCIEDHQAOLTVNRFTQTG 504
QY 481 GVSLSGNAVLSCYKNGAGNSASNAITLKHIGLNLSSILKSGAEIPLLVPEPTNNSNY 540
DB 505 GVSLSGNAVLSCYKNGAGNSASNAITLKHIGLNLSSILKSGAEIPLLVPEPTNNSNY 564
QY 541 TADTAATFSLSDVKLSLIDYDGNPSYESTDLTHALSSQPMLSISEASDNOLRSDMDFSG 600
DB 565 TADTAATFSLSDVKLSLIDYDGNPSYESTDLTHALSSQPMLSISEASDNOLRSDMDFSG 624
QY 601 LNPVHYCQGLWGWAKTQDPEPASSATITDPKANRFRHTLLTLWLPAGYVPSPKHRS 660
DB 625 LNPVHYCQGLWGWAKTQDPEPASSATITDPKANRFRHTLLTLWLPAGYVPSPKHRS 684
QY 661 PLIANTLWGNMLLATESLKSNAELTPSDHPFWGITGGGLGMVYQDPRENHFGFHMRSRG 720
DB 685 PLIANTLWGNMLLATESLKSNAELTPSDHPFWGITGGGLGMVYQDPRENHFGFHMRSRG 744
QY 721 YSAGMIAGQHTFSLKFSQYTKLNERYAKNNVSSKNYSCQGMFLSLQEGFLTLKLVL 780
DB 745 YSAGMIAGQHTFSLKFSQYTKLNERYAKNNVSSKNYSCQGMFLSLQEGFLTLKLVL 804
QY 781 YSYGDHNCHEFTYQGENLTSQGTFRSQTMGGAFFDLPMPKPFGSTHILTAFLGALGIYS 840
DB 805 YSYGDHNCHEFTYQGENLTSQGTFRSQTMGGAFFDLPMPKPFGSTHILTAFLGALGIYS 864
QY 841 SLSHFTVEGAPRFSFTKTLINVLVPIGVKGSFMMNATQRPQAWTVBLAYQVLYROEPG 900
DB 865 SLSHFTVEGAPRFSFTKTLINVLVPIGVKGSFMMNATQRPQAWTVBLAYQVLYROEPG 924
QY 901 IATOLLASKGIWFGSGSPSSRRHMSYKISQOTQPLSWLTLHFQYHGYSSTFCNYLNGE 960
DB 925 IATOLLASKGIWFGSGSPSSRRHMSYKISQOTQPLSWLTLHFQYHGYSSTFCNYLNGE 984
QY 961 IALRF 965
DB 985 IALRF 989

RESULT 3

AAB13634
ID AAB13634 standard; Protein; 964 AA.
XX
AC AAB13634;
XX
DT 02-FEB-2001 (first entry)
XX
DE C. trachomatis pmpE gene protein.
XX
KW Chlamydial infection; sexually transmitted disease;
KW pelvic inflammatory disease; PID; tubal obstruction; infertility;
KW trachoma; blindness; acute respiratory tract infection;
KW atherosclerosis; coronary heart disease; antibacterial.
XX
OS Chlamydia trachomatis.
XX
PN W0200034483-A2.
XX
PD 15-JUN-2000.
XX
PF 08-DEC-1999; 99WO-US29012.
XX
PR 08-DEC-1998; 98US-0208277.
PR 08-APR-1999; 99US-0288594.
PR 01-OCT-1999; 99US-0410568.
PR 22-OCT-1999; 99US-0426571.
XX
PA (CORI-) CORIXA CORP.
PI
PI Probst P, Bhatia A, Skeiky YAW, Fling SP, Jen S, Stromberg EJ;
XX
XX WPI; 2000-431303/37.
XX
XX Isolated polypeptide for diagnosis and treatment of Chlamydia infection
PT comprises immunogenic portion of Chlamydia antigen, which comprises
PT amino acid sequence encoded by polynucleotide sequence -
XX
XX Claim 2; Pages 184-186; 256pp; English.
XX
CC The present invention relates to new nucleic acid sequences and the
CC proteins encoded by the nucleic acid sequences. The encoded proteins
CC comprise an immunogenic portion of a Chlamydia antigen. The encoded
CC proteins are useful for the serodiagnosis and treatment of Chlamydia
CC infection. Chlamydiae are intracellular bacterial pathogens that are
CC responsible for a wide variety of human infections. C. trachomatis
CC infection is one of the most common sexually transmitted diseases and can
CC lead to pelvic inflammatory disease (PID), resulting in tubal obstruction
CC and infertility. Trachoma due to ocular infection with C. trachomatis is
CC the leading cause of preventable blindness worldwide. C. pneumoniae is a
CC major cause of acute respiratory tract infections in humans and is also
CC thought to play a role in the pathogenesis of atherosclerosis and
CC coronary heart disease. The present sequence is a protein isolated in the
CC present invention.
XX
SQ Sequence 964 AA;
Query Match 98.2%; Score 4994.5; DB 21; Length 964;
Best Local Similarity 98.4%; Pred. No. 0;
Matches 950; Conservative 7; Mismatches 7; Indels 1; Gaps 1;
QY 1 MKKAFFFLIGNSLGLAREVPSRIFLMPNSVDPPTKESLSNKISLGLDTHNLTCYLDN 60
DB 1 MKKAFFFLIGNSLGLAREVPSRIFLMPNSVDPPTKESLSNKISLGLDTHNLTCYLDN 60
QY 61 LRYLAILQKTPNEGAATITDYLSPFDQKEGIYFAKNLTPESGGAIGYASPNPVEI 120
DB 61 LRYLAILQKTPNEGAATITDYLSPFDQKEGIYFAKNLTPESGGAIGYASPNPVEI 120
QY 121 RDTIGPVIFENNTCCRPFTSSNPNAAVNKIREGAIHAQNLYINHNHVVGVGFMKFSYVR 180
DB 121 RDTIGPVIFENNTCCRPFTSSNPNAAVNKIREGAIHAQNLYINHNHVVGVGFMKFSYVR 179
QY 181 GGAISTANTFVWSNQCFLFMDNICIQTNTAGKGGAIYAGTSNFSFNCDLFFINNAC 240

Db 180 GGAISTANTFVYSENOQSCFLFMDNICIQNTAGKGAIYAGTSNFSFNCCDLFFINNAC 239
Qy 241 CAGGAIFSPICSLTGNRGNIVFYNNRCFKNVETASSEADGGAIKVTTRLDVTVGNRGRIF 300
Db 240 CAGGAIFSPICSLTGNRGNIVFYNNRCFKNVETASSEADGGAIKVTTRLDVTVGNRGRIF 299
Qy 301 FSDNITKNYGGAIYAPVTVLDVNGPTYFNNIANNKGGAIYIDGTSNKSISADRHAIIFN 360
Db 300 FSDNITKNYGGAIYAPVTVLDVNGPTYFNNIANNKGGAIYIDGTSNKSISADRHAIIFN 359
Qy 361 ENIVNTNANGTSTSANPPRRNAITVASSSGEILLGAGSSONLIFYDPIEVSNAGVSYS 420
Db 360 ENIVNTNANGTSTSANPPRRNAITVASSSGEILLGAGSSONLIFYDPIEVSNAGVSYS 419
Qy 421 FNKEADQTSVVFSGATVNSADFHQRNLQTKTPAPLTLSNGFLCIEDHQAQLTVNRFTQTG 480
Db 420 FNKEADQTSVVFSGATVNSADFHQRNLQTKTPAPLTLSNGFLCIEDHQAQLTVNRFTQTG 479
Qy 481 GVVSLGNGAVLSYCKNGKNGAGNSASNASITLKHIGLNLSSILKSGAEIPLLLWVEPTNNSNY 540
Db 480 GVVSLGNGAVLSYCKNGKNGAGNSASNASITLKHIGLNLSSILKSGAEIPLLLWVEPTNNSNY 539
Qy 541 TADTAATFSLSDVKLSLIDYGNPSYESTDLTHALSSQPMLSISEASONQLRSDDMDFSG 600
Db 540 TADTAATFSLSDVKLSLIDYGNPSYESTDLTHALSSQPMLSISEASONQLRSDDMDFSG 599
Qy 601 LNVPHYGWGLTWGAKTQDPEPASSATITDPQKANRFRHRTLLLTWLPAGVYVSPKHS 660
Db 600 LNVPHYGWGLTWGAKTQDPEPASSATITDPQKANRFRHRTLLLTWLPAGVYVSPKHS 659
Qy 661 PLIANTLWGNMLLATYSLKNSAELPSPDHPFWGITGGGLGMVYODPPRENHFGFHRSSG 720
Db 660 PLIANTLWGNMLLATYSLKNSAELPSPDHPFWGITGGGLGMVYODPPRENHFGFHRSSG 719
Qy 721 YSAGMIAGTHTFSLKFSQTYTKLNERYAKNNVSSKNYSCQGMFLFSLQEGFLTLKLVL 780
Db 720 YSAGMIAGTHTFSLKFSQTYTKLNERYAKNNVSSKNYSCQGMFLFSLQEGFLTLKLVL 779
Qy 781 YSYGDHNCHEFTOGENLTSGTFSQTMGGAVFEDLPKPGSTHILTAFLGALGIYS 840
Db 780 YSYGDHNCHEFTOGENLTSGTFSQTMGGAVFEDLPKPGSTHILTAFLGALGIYS 839
Qy 841 SLSHTEVGAYPRSESTKTPNLNLVPIGVKGFSEFNATQRPQAWVELAYQVLYRQBP 900
Db 840 SLSHTEVGAYPRSESTKTPNLNLVPIGVKGFSEFNATQRPQAWVELAYQVLYRQBP 899
Qy 901 IATQLLASKGIWFGSGSPSSRRHMSYKISQQTQPLSWTLTHFQYHGFYSSSTFCNYLNGE 960
Db 900 IATQLLASKGIWFGSGSPSSRRHMSYKISQQTQPLSWTLTHFQYHGFYSSSTFCNYLNGE 959
Qy 961 IALRF 965
Db 960 IALRF 964

RESULT 4

AAG83202

ID AAG83202 standard; Protein: 964 AA.

XX AC AAG83202;

XX AC AAG83202;

XX 05-SEP-2001 (first entry)

XX Protein encoded by Chlamydia trachomatis pmpE gene.

XX Chlamydia; vaccine; infection; fusion protein; antigen;
KW pelvic inflammatory disease; trachoma; atherosclerosis; heart disease;
KW acute respiratory tract infection; Cap1; CT529; OMCB;
KW polymorphic membrane protein; pmp; thiol specific antioxidant; TSA.
XX Chlamydia trachomatis.
OS XX

PN WO200140474-A2.
XX 07-JUN-2001.
XX 04-DEC-2000; 2000WO-US32919.
XX 03-DEC-1999; 99US-0454684.
PR 19-APR-2000; 2000US-0556877.
PR 20-JUN-2000; 2000US-0598419.
XX (CORI-) CORIXA CORP.
XX Probst P, Bhatia A, Skeiky YAW, Fling SP, Scholler J;
XX WPI; 2001-374831/39.
XX Chlamydia polypeptides and fusion proteins useful for preventing pelvic
PT inflammatory disease, trachoma, acute respiratory tract infections,
PT atherosclerosis and heart disease -
XX Claim 2; Page 191-193; 295pp; English.
XX The present sequence is provided in a specification relating to
CC compounds and methods for the treatment and diagnosis of chlamydial
CC infection. The compounds provided include polypeptides and fusion
CC proteins comprising immunogenic portions of Chlamydia antigens
CC and DNA sequences encoding such polypeptides. They are useful for
CC vaccinating against chlamydial infection, which causes pelvic
CC inflammatory disease, trachoma, acute respiratory tract infections,
CC atherosclerosis and heart disease.
XX SQ Sequence 964 AA;

Query Match 98.2%; Score 4994.5; DB 22; Length 964;
Best Local Similarity 98.4%; Pred. No. 0;
Matches 950; Conservative 7; Mismatches 7; Indels 1; Gaps 1;

Qy 1 MKKAFFFLIGNSLGLAREVPSRIFLMPNSVPDPTKESLSNKISLTGDTNLTNCYLDN 60
Db 1 MKKAFFFLIGNSLGLAREVPSRIFLMPNSVPDPTKESLSNKISLTGDTNLTNCYLDN 60
Qy 61 LRYILAILOKTPNEGAAYTITDYLSEFFDTQKEGIVFAKNLTPESGGAIGYASPNPTVEI 120
Db 61 LRYILAILOKTPNEGAAYTITDYLSEFFDTQKEGIVFAKNLTPESGGAIGYASPNPTVEI 120
Qy 121 RDTIGPVIFENNTCCRPFTSSNPNAVNKIREGGAIHAQNLINHNHVDVGFMKNFYSVR 180
Db 121 RDTIGPVIFENNTCCRPFTSSNPNAVNKIREGGAIHAQNLINHNHVDVGFMKNFYSVR 179
Qy 181 GGAISTANTFVYSENOQSCFLFMDNICIQNTAGKGAIYAGTSNFSFNCCDLFFINNAC 240
Db 180 GGAISTANTFVYSENOQSCFLFMDNICIQNTAGKGAIYAGTSNFSFNCCDLFFINNAC 239
Qy 241 CAGGAIFSPICSLTGNRGNIVFYNNRCFKNVETASSEADGGAIKVTTRLDVTVGNRGRIF 300
Db 240 CAGGAIFSPICSLTGNRGNIVFYNNRCFKNVETASSEADGGAIKVTTRLDVTVGNRGRIF 299
Qy 301 FSDNITKNYGGAIYAPVTVLDVNGPTYFNNIANNKGGAIYIDGTSNKSISADRHAIIFN 360
Db 300 FSDNITKNYGGAIYAPVTVLDVNGPTYFNNIANNKGGAIYIDGTSNKSISADRHAIIFN 359
Qy 361 ENIVNTNANGTSTSANPPRRNAITVASSSGEILLGAGSSONLIFYDPIEVSNAGVSYS 420
Db 360 ENIVNTNANGTSTSANPPRRNAITVASSSGEILLGAGSSONLIFYDPIEVSNAGVSYS 419
Qy 421 FNKEADQTSVVFSGATVNSADFHQRNLQTKTPAPLTLSNGFLCIEDHQAQLTVNRFTQTG 480
Db 420 FNKEADQTSVVFSGATVNSADFHQRNLQTKTPAPLTLSNGFLCIEDHQAQLTVNRFTQTG 479
Qy 481 GVVSLGNGAVLSYCKNGKNGAGNSASNASITLKHIGLNLSSILKSGAEIPLLLWVEPTNNSNY 540
Db 480 GVVSLGNGAVLSYCKNGKNGAGNSASNASITLKHIGLNLSSILKSGAEIPLLLWVEPTNNSNY 539

QY 541 TADTAATFSLSDVKLSLIDYGNPSYESTDLTHALSSQPMLSISEASDNLRSDDMFSG 600
Db 540 TADTAATFSLSDVKLSLIDYGNPSYESTDLTHALSSQPMLSISEASDNLQSENIIDFSG 599
QY 601 LNPVHYGQGLWTGWAKTQDPEPASSATITDPQKANRFRHTLLTLWLPAGYVSPKHS 660
Db 600 LNPVHYGQGLWTGWAKTQDPEPASSATITDPQKANRFRHTLLTLWLPAGYVSPKHS 659
QY 661 PLIANTLWGNMMLLATESLKNSAELTSPDHFPWGITGGGLGMVYQDPRENHPGFHMRSSG 720
Db 660 PLIANTLWGNMMLLATESLKNSAELTSPGHFPWGITGGGLGMVYQDPRENHPGFHMRSSG 719
QY 721 YSAGMIAGQTHFTSLKFSQTYTKLNERAKNNVSSKNYSQCGEMLSLQSGFLTLKLVL 780
Db 720 YSAGMIAGQTHFTSLKFSQTYTKLNERAKNNVSSKNYSQCGEMLSLQSGFLTLKLVL 779
QY 781 YSGDHNCHHFTYQGENLTSGQTRFRTMGGAFFDLPMPKPGFSTHILTAFFLGALGIYS 840
Db 780 YSGDHNCHHFTYQGENLTSGQTRFRTMGGAFFDLPMPKPGFSTHILTAFFLGALGIYS 839
QY 841 SLSHFTEVGAYPRSFSTKTPLINVLVPIGVKGSFMMNATORQAWTVELAYQVLYRQEPG 900
Db 840 SLSHFTEVGAYPRSFSTKTPLINVLVPIGVKGSFMMNATORQAWTVELAYQVLYRQEPG 899
QY 901 IATQLLASKGIWFGSGSPSSRRHMSYKISQOTPLSLWTLHFQYHGFYSSTFCNYLNGE 960
Db 900 IATQLLASKGIWFGSGSPSSRRHMSYKISQOTPLSLWTLHFQYHGFYSSTFCNYLNGE 959
QY 961 IALRF 965
Db 960 IALRF 964

RESULT 5
ABB94173
ID ABB94173 standard; Protein; 964 AA.
XX ABB94173;
XX
XX
XX 05-JUN-2002 (first entry)
XX Chlamydia protein sequence SEQ ID NO:177.
XX
XX Chlamydial infection; Chlamydia; vaccine; detection; diagnosis;
XX antigen; antibacterial; immunostimulant; immune response;
XX Chlamydia-specific T-cell response.
XX
XX Chlamydia sp.
XX W0200208267-A2.
XX
XX 31-JAN-2002.
XX
XX 20-JUL-2001; 2001WO-US23121.
XX
XX 20-JUL-2000; 2000US-0620412.
XX 23-APR-2001; 2001US-0841132.
XX
XX (CORI-) CORIXA CORP.
XX
XX Fling SP, Skeiky YAW, Probst P, Bhatia A;
XX WPI; 2002-179901/23.
XX
XX Novel compositions comprising Chlamydia CapI protein and its use in the
XX treatment of Chlamydia infection.
XX
XX Example 1; Page 223-225; 537pp; English.
XX
XX The present invention describes compositions comprising a Chlamydia CapI
XX protein and methods for the diagnosis and therapy of Chlamydia infection.
XX Chlamydia DNA and protein sequences from the present invention can have
XX antibacterial and immunostimulant activities, and can be used in

CC vaccines. Compounds from the present invention can be used for eliciting
CC an immune response, specifically stimulating a Chlamydia-specific T-cell
CC response or inhibiting the development of a Chlamydia infection in an
CC animal. Methods from the present invention can be used: for detecting the
CC presence of Chlamydia in a patient; to stimulate and/or expand T cells
CC specific for a Chlamydia protein; and for treatment of a Chlamydia
CC infection. ABL92394 to ABL92709 and ABB94096 to ABB94374 represent
CC sequences used in the exemplification of the present invention.
XX
SQ Sequence 964 AA;
Query Match 98.2%; Score 4994.5; DB 23; Length 964;
Best Local Similarity 98.4%; Pred. No. 0;
Matches 950; Conservative 7; Mismatches 7; Indels 1; Gaps 1;
QY 1 MKKAFFFLLGNSLSGLAREVPSRIFLMPNSVPDPPTKESLSNKISLTGDTHTNLTNCYLDN 60
Db 1 MKKAFFFLLGNSLSGLAREVPSRIFLMPNSVPDPPTKESLSNKISLTGDTHTNLTNCYLDN 60
QY 61 LRYLAILQKTPNEGAAVTITDYLSPFDTOKEGIYFAKNTLPESGGAIGVYASNPSTVEI 120
Db 61 LRYLAILQKTPNEGAAVTITDYLSPFDTOKEGIYFAKNTLPESGGAIGVYASNPSTVEI 120
QY 121 RDTIGPVIFENNCCRPFTSSNPAAVNKIREGGAHQAQNLINHNHVDVYVGMKNSFYVR 180
Db 121 RDTIGPVIFENNCCRPFTSSNPAAVNKIREGGAHQAQNLINHNHVDVYVGMKNSFYVR 179
QY 181 GGAISTANTFVVENOSCFIFMDNICIQTNAGKGGAIYAGTNSPESNCDLFFINAC 240
Db 180 GGAISTANTFVVENOSCFIFMDNICIQTNAGKGGAIYAGTNSPESNCDLFFINAC 239
QY 241 CAGGAIFSPICSLTGNRGNTVEYNNRCFKNVETASSPASDGAITKTRLDVTDGNRGRIF 300
Db 240 CAGGAIFSPICSLTGNRGNTVEYNNRCFKNVETASSPASDGAITKTRLDVTDGNRGRIF 299
QY 301 FSDNITKNYGGAIYAPVVTLVNDNGPTVFYINNIANNKGAIYIDGTSNKSISADRAHAI 360
Db 300 FSDNITKNYGGAIYAPVVTLVNDNGPTVFYINNIANNKGAIYIDGTSNKSISADRAHAI 359
QY 361 ENIVTNVTNANGTSTSANPPRNATVASSSGEILLGAGSSQNLIFYDPIEVSNAGVS 420
Db 360 ENIVTNVTNANGTSTSANPPRNATVASSSGEILLGAGSSQNLIFYDPIEVSNAGVS 419
QY 421 FKEADQTSVFSFGATVNSADFHQRLQKTPAPLTSLNGFLCIEDHAOLTVNRFTQTG 480
Db 420 FKEADQTSVFSFGATVNSADFHQRLQKTPAPLTSLNGFLCIEDHAOLTVNRFTQTG 479
QY 481 GVVSLGNGAVLSYKNGAGNSASNTLKHIGLNLSSILKSGAEIPLLWPEPTNNSNY 540
Db 480 GVVSLGNGAVLSYKNGAGNSASNTLKHIGLNLSSILKSGAEIPLLWPEPTNNSNY 539
QY 541 TADTAATFSLSDVKLSLIDYGNPSYESTDLTHALSSQPMLSISEASDNLRSDDMFSG 600
Db 540 TADTAATFSLSDVKLSLIDYGNPSYESTDLTHALSSQPMLSISEASDNLQSENIIDFSG 599
QY 601 LNPVHYGQGLWTGWAKTQDPEPASSATITDPQKANRFRHTLLTLWLPAGYVSPKHS 660
Db 600 LNPVHYGQGLWTGWAKTQDPEPASSATITDPQKANRFRHTLLTLWLPAGYVSPKHS 659
QY 661 PLIANTLWGNMMLLATESLKNSAELTSPDHFPWGITGGGLGMVYQDPRENHPGFHMRSSG 720
Db 660 PLIANTLWGNMMLLATESLKNSAELTSPGHFPWGITGGGLGMVYQDPRENHPGFHMRSSG 719
QY 721 YSAGMIAGQTHFTSLKFSQTYTKLNERAKNNVSSKNYSQCGEMLSLQSGFLTLKLVL 780
Db 720 YSAGMIAGQTHFTSLKFSQTYTKLNERAKNNVSSKNYSQCGEMLSLQSGFLTLKLVL 779
QY 781 YSGDHNCHHFTYQGENLTSGQTRFRTMGGAFFDLPMPKPGFSTHILTAFFLGALGIYS 840
Db 780 YSGDHNCHHFTYQGENLTSGQTRFRTMGGAFFDLPMPKPGFSTHILTAFFLGALGIYS 839
QY 841 SLSHFTEVGAYPRSFSTKTPLINVLVPIGVKGSFMMNATORQAWTVELAYQVLYRQEPG 900
Db 841 SLSHFTEVGAYPRSFSTKTPLINVLVPIGVKGSFMMNATORQAWTVELAYQVLYRQEPG 900

Db 840 SLSHTEVGA YPRSRSTKTPPLINLVPIGVKGSFNMNATHRPOAWTVLAYQPVLYRQBP 899
 QY 901 IATQLLASKGIWFGSGSPSSRHMSYKISQQTQPLSWLTLLHFQYHGFYSSSTFCNYLNGE 960
 Db 900 IATQLLASKGIWFGSGSPSSRHMSYKISQQTQPLSWLTLLHFQYHGFYSSSTFCNYLNGE 959
 QY 961 IALRF 965
 Db 960 IALRF 964

RESULT 6

AAB13640
 ID AAB13640 standard; Protein: 977 AA.

XX AAB13640;

DT 02-FEB-2001 (first entry)

DE C. trachomatis pmpE gene amino terminus minus signal sequence protein.

KW Chlamydial infection; sexually transmitted disease;

KW pelvic inflammatory disease; PID; tubal obstruction; infertility;

KW trachoma; blindness; acute respiratory tract infection;

KW atherosclerosis; coronary heart disease; antibacterial.

XX Chlamydia trachomatis.

PN W0200034483-A2.

XX 15-JUN-2000.

XX 08-DEC-1999; 99WO-US29012.

PR 08-DEC-1998; 98US-0208277.

PR 01-OCT-1999; 99US-0288594.

PR 22-OCT-1999; 99US-0410568.

XX (CORI-) CORIXA CORP.

PI Probst P, Bhatia A, Skeiky YAW, Fling SP, Jen S, Stromberg EJ;
 DR WPI; 2000-431303/37.

XX Isolated polypeptide for diagnosis and treatment of Chlamydia infection
 PT comprises immunogenic portion of Chlamydia antigen, which comprises
 PT amino acid sequence encoded by polynucleotide sequence -
 XX Claim 2; Pages 210-212; 256pp; English.

XX The present invention relates to new nucleic acid sequences and the
 CC proteins encoded by the nucleic acid sequences. The encoded proteins
 CC comprise an immunogenic portion of a Chlamydia antigen. The encoded
 CC proteins are useful for the serodiagnosis and treatment of Chlamydia
 CC infection. Chlamydiae are intracellular bacterial pathogens that are
 CC responsible for a wide variety of human infections. C. trachomatis
 CC infection is one of the most common sexually transmitted diseases and can
 CC lead to pelvic inflammatory disease (PID), resulting in tubal obstruction
 CC and infertility. Trachoma due to ocular infection with C. trachomatis is
 CC the leading cause of preventable blindness worldwide. C. pneumoniae is a
 CC major cause of acute respiratory tract infections in humans and is also
 CC thought to play a role in the pathogenesis of atherosclerosis and
 CC coronary heart disease. The present sequence is a protein isolated in the
 CC present invention.

XX Sequence 977 AA;

Query Match 96.7%; Score 4919.5; DB 21; Length 977;
 Best Local Similarity 98.4%; Pred. No. 0;
 Matches 935; Conservative 7; Mismatches 7; Indels 1; Gaps 1;

QY 16 GLAREVPSRIFLMPNSVDPPTKESLNKISLTGDTNLTNCYLDNRLYLAILQKTPNEG 75

Db 29 GLAREVPSRIFLMPNSVDPPTKESLNKISLTGDTNLTNCYLDNRLYLAILQKTPNEG 88
 QY 76 AAVTTIDTSLSDFTQKEGIYFAKNLTPESSGAIGVYASNSPTVEIRDITGPIVRENNTCC 135
 Db 89 AAVTTIDTSLSDFTQKEGIYFAKNLTPESSGAIGVYASNSPTVEIRDITGPIVRENNTCC 148
 QY 136 RPTSSNPAAVNKIREGGAHAQNLXINHNDVVGFMKNFSYVGGAIATANTFVVSSEN 195
 Db 149 RLFTWRNPFYAA-DKIREGGAHAQNLXINHNDVVGFMKNFSYVGGAIATANTFVVSSEN 207
 QY 196 QSCFLFMDNICIQNTAGKGAIYAGTSNFSFNNDLFFINNACCAGAIATANTFVVSSEN 255
 Db 208 QSCFLFMDNICIQNTAGKGAIYAGTSNFSFNNDLFFINNACCAGAIATANTFVVSSEN 267
 QY 256 NRGNTVFYNNRCFKNVETASSEASDGGAIKVTTRLDVTGNRGRIFFSNITKNYGGAIYA 315
 Db 268 NRGNTVFYNNRCFKNVETASSEASDGGAIKVTTRLDVTGNRGRIFFSNITKNYGGAIYA 327
 QY 316 PVVTLVDNGPTFYFNNIANNKGGAIYIDGTSNKSISADRHAIIFENIVTVNVTNANGTST 375
 Db 328 PVVTLVDNGPTFYFNNIANNKGGAIYIDGTSNKSISADRHAIIFENIVTVNVTNANGTST 387
 QY 376 SANPPRRNAITVASSSGEILLGAGSSQNLIFYDPIEVSNAAGVSFNFKEADQTSVWFSG 435
 Db 388 SANPPRRNAITVASSSGEILLGAGSSQNLIFYDPIEVSNAAGVSFNFKEADQTSVWFSG 447
 QY 436 ATVNSADPHQNLQTKTPAPLTLNSGFLCIEDHAQLTVNRFTQGGVYSLNGAVLSYCK 495
 Db 448 ATVNSADPHQNLQTKTPAPLTLNSGFLCIEDHAQLTVNRFTQGGVYSLNGAVLSYCK 507
 QY 496 NGAGNSASNASITLKHIGLNLSLILKSGAEIPLLWVEPTNNSNNTADTAATFSLSDVKL 555
 Db 508 NGTGDASNASITLKHIGLNLSLILKSGAEIPLLWVEPTNNSNNTADTAATFSLSDVKL 567
 QY 556 SLIDDYGNSPYESTDLTHALSSQPMLSISEASDNOLRSDDDMFSGLNVPVHYGWOGLWTWG 615
 Db 568 SLIDDYGNSPYESTDLTHALSSQPMLSISEASDNOLRSDDDMFSGLNVPVHYGWOGLWTWG 627
 QY 616 WAKTQDPEPASSATITDPOKANRFRHTLLTLWLPAGVYVPSPKHRSPLTANTLWGNMLLAT 675
 Db 628 WAKTQDPEPASSATITDPOKANRFRHTLLTLWLPAGVYVPSPKHRSPLTANTLWGNMLLAT 687
 QY 676 ESLKNSAELTSPDHPFWGITGGGLGMVYQDPRENHPGFHMRSSGYSAGMIAGQTHFTSL 735
 Db 688 ESLKNSAELTSPDHPFWGITGGGLGMVYQDPRENHPGFHMRSSGYSAGMIAGQTHFTSL 747
 QY 736 KFSQTYTKLNERYAKNNVSSKNYSCQGMELFSLQEGFLLTKLVGLYSYGDHNCHEFTYQG 795
 Db 748 KFSQTYTKLNERYAKNNVSSKNYSCQGMELFSLQEGFLLTKLVGLYSYGDHNCHEFTYQG 807
 QY 796 ENLTSQGTFRSQTGGAFFDLPMPKPGSTHILTAFFLALGALYSSLSHFTVEGAYPRSF 855
 Db 808 ENLTSQGTFRSQTGGAFFDLPMPKPGSTHILTAFFLALGALYSSLSHFTVEGAYPRSF 867
 QY 856 STKTPLINLVPIGVKGSFNMNATHRPOAWTVLAYQPVLYRQBPATQLLASKGIWFGS 915
 Db 868 STKTPLINLVPIGVKGSFNMNATHRPOAWTVLAYQPVLYRQBPATQLLASKGIWFGS 927
 QY 916 GSPSSRHMSYKISQQTQPLSWLTLLHFQYHGFYSSSTFCNYLNGEIALRF 965
 Db 928 GSPSSRHMSYKISQQTQPLSWLTLLHFQYHGFYSSSTFCNYLNGEIALRF 977

RESULT 7

AAG83208
 ID AAG83208 standard; Protein: 977 AA.

XX AAG83208;

DT 05-SEP-2001 (first entry)

DE Protein encoded by Chlamydia trachomatis pmpE gene.

Chlamydia; vaccine; infection; fusion protein; antigen; pelvic inflammatory disease; trachoma; atherosclerosis; heart disease; acute respiratory tract infection; Capl; CTS29; OMCB; polymorphic membrane protein; pmp; thiol specific antioxidant; TSA. Chlamydia trachomatis. WO200140474-A2. 07-JUN-2001. 04-DEC-2000; 2000WO-US32919. 03-DEC-1999; 99US-0454684. 19-APR-2000; 2000US-0556877. 20-JUN-2000; 2000US-0598419. (CORI-) CORIXA CORP. Probst P, Bhatia A, Skeiky YAW, Fling SP, Scholler J; WPI; 2001-374831/39. Chlamydia polypeptides and fusion proteins useful for preventing pelvic inflammatory disease, trachoma, acute respiratory tract infections, atherosclerosis and heart disease - Claim 2; Page 216-218; 295pp; English. The present sequence is provided in a specification relating to compounds and methods for the treatment and diagnosis of chlamydial infection. The compounds provided include polypeptides and fusion proteins comprising immunogenic portions of Chlamydia antigens and DNA sequences encoding such polypeptides. They are useful for vaccinating against chlamydial infection, which causes pelvic inflammatory disease, trachoma, acute respiratory tract infections, atherosclerosis and heart disease. Sequence 977 AA; Query Match 96.7%; Score 4919.5; DB 22; Length 977; Best Local Similarity 98.4%; Pred. No. 0; Matches 935; Conservative 7; Mismatches 7; Indels 1; Gaps 1; 16 GLAREVPSRIFLMPNSVPDPTKESLNKISLTGDTNLTNLYLILAILOKTPNEG 75 29 GLAREVPSRIFLMPNSVPDPTKESLNKISLTGDTNLTNLYLILAILOKTPNEG 88 76 AAVTITDYLSTFDTQREGIYFAKNLTPESGGAIGYASPNSTVEIRDTIGPVIFENNTCC 135 89 AAVTITDYLSTFDTQREGIYFAKNLTPESGGAIGYASPNSTVEIRDTIGPVIFENNTCC 148 136 RPTSSNPNAVNKIREGGAIHQALYINHNHVDVGMKFNFSYVRGAISTANTFVYSEN 195 149 RLFTWRNPYAA-DKIREGGAIHQALYINHNHVDVGMKFNFSYVRGAISTANTFVYSEN 207 196 QSCFLFMDNICIOTNAGKGAIYAGTSNFSFNNDLFFINNACCAGGAIFSPICSLTG 255 208 QSCFLFMDNICIOTNAGKGAIYAGTSNFSFNNDLFFINNACCAGGAIFSPICSLTG 267 256 NRGNIYVNNRCFKNVETASSEASDGAIKVTRLDVGNRGRIFTSNITKNYGAIYA 315 268 NRGNIYVNNRCFKNVETASSEASDGAIKVTRLDVGNRGRIFTSNITKNYGAIYA 327 316 PVTVLDNGPTYFINNIANNKGAIYIDGTSNKSISADRHAIIFNENIVTNVTNANGTST 375 328 PVTVLDNGPTYFINNIANNKGAIYIDGTSNKSISADRHAIIFNENIVTNVTNANGTST 387 376 SANPPRRNAITVASSGEILLGAGSSONLIIFYDPIEVSNAGVSFNKEADQGTGVVFSG 435 388 SANPPRRNAITVASSGEILLGAGSSONLIIFYDPIEVSNAGVSFNKEADQGTGVVFSG 447

436 ATVNSADFHORNLQTKTAPLTLNSNGFLCTIEDHAQLTVNRFOTQGGVYSLGNGAVLSCKY 495 448 ATVNSADFHORNLQTKTAPLTLNSNGFLCTIEDHAQLTVNRFOTQGGVYSLGNGAVLSCKY 507 496 NGAGNSASNAITLKHIGLNLSSILKSGAEIPLLWVEPTNNSNNYTDATATFSLSDVKL 555 508 NGTGDASASNAITLKHIGLNLSSILKSGAEIPLLWVEPTNNSNNYTDATATFSLSDVKL 567 556 SLIDDDYGNPSYESTDLTHALSSOPMLSISEASDNQLRSDDMDFSGLNVPHYGQGLWTWG 615 568 SLIDDDYGNPSYESTDLTHALSSOPMLSISEASDNQLRSDDMDFSGLNVPHYGQGLWTWG 627 616 WAKTQDPEPASSATITDPQKANRFHRTLLTLWLPAGVVPSPKHSRPLIANTLGNMLLAT 675 628 WAKTQDPEPASSATITDPQKANRFHRTLLTLWLPAGVVPSPKHSRPLIANTLGNMLLAT 687 676 ESLKNSAELTPSDHPFWGITGGGLGMVMYODPRENHPGFHMRSSGYSGAGIAGTHTFSL 735 688 ESLKNSAELTPSGHPFWGITGGGLGMVMYODPRENHPGFHMRSSGYSGAGIAGTHTFSL 747 736 KFSQTYTKLNERYAKNNVSSKNYSCOGEMLFSLQEGFLTKLVGLYSYGDHNCHEFTQG 795 748 KFSQTYTKLNERYAKNNVSSKNYSCOGEMLFSLQEGFLTKLVGLYSYGDHNCHEFTQG 807 796 ENLTSGTFRSQTMGGAVFFDLPMKPFGSTHILTAFLGALGIYSSLSHFTEVGAYPRSF 855 808 ENLTSGTFRSQTMGGAVFFDLPMKPFGSTHILTAFLGALGIYSSLSHFTEVGAYPRSF 867 856 STKTPLINLVLPICGVKSGFNNATQPOAWTVELAYQPVLYRQEPGIATQLLASKGIWFGS 915 868 STKTPLINLVLPICGVKSGFNNATQPOAWTVELAYQPVLYRQEPGIATQLLASKGIWFGS 927 916 GSPSSRRHMSYKISQQTQPLSWLTHFOYHGFYSSSTFCNLYNGETALRF 965 928 GSPSSRRHMSYKISQQTQPLSWLTHFOYHGFYSSSTFCNLYNGETALRF 977 RESULT 8 ABB94179 ID ABB94179 standard; Protein; 977 AA. XX AC ABB94179; XX DT 05-JUN-2002 (first entry) XX DE Chlamydia protein sequence SEQ ID NO:191. XX KW Chlamydial infection; Chlamydia; vaccine; detection; diagnosis; antigen; antibacterial; immunostimulant; immune response; Chlamydia-specific T-cell response. XX OS Chlamydia sp. XX PN WO200208267-A2. XX PD 31-JAN-2002. XX PF 20-JUL-2001; 2001WO-US23121. XX PR 20-JUL-2000; 2000US-0620412. PR 23-APR-2001; 2001US-0841132. XX PA (CORI-) CORIXA CORP. XX PI Fling SP, Skeiky YAW, Probst P, Bhatia A; XX WPI; 2002-179901/23. XX PT Novel compositions comprising Chlamydia Capl protein and its use in the treatment of Chlamydia infection - XX PS Example 1; Page 247-249; 537pp; English. XX

CC The present invention describes compositions comprising a Chlamydia Cap1
CC protein and methods for the diagnosis and therapy of Chlamydia infection.
CC Chlamydia DNA and protein sequences from the present invention can have
CC antibacterial and immunostimulant activities, and can be used in
CC vaccines. Compounds from the present invention can be used for eliciting
CC an immune response, specifically stimulating a Chlamydia-specific T-cell
CC response or inhibiting the development of a Chlamydia infection in an
CC animal. Methods from the present invention can be used for detecting the
CC presence of Chlamydia in a patient; to stimulate and/or expand T cells
CC specific for a Chlamydia protein; and for treatment of a Chlamydia
CC infection. ABL92394 to ABL92709 and ABB94096 to ABB94374 represent
CC sequences used in the exemplification of the present invention.
XX
SQ

Query Match	96.7%;	Score 4919.5;	DB 23;	Length 977;
Best Local Similarity	98.4%;	Pred. No. 0;		
Matches 935;	Conservative 7;	Mismatches 7;	Indels 1;	Gaps 1;
QY	16	GLAREVPSRIFLMPNSVDPPTKESLSNKISLTGDTNHLTNCYLDNLRYLAILQKTPNEG	75	
DB	29	GLAREVPSRIFLMPNSVDPPTKESLSNKISLTGDTNHLTNCYLDNLRYLAILQKTPNEG	88	
QY	76	AAVTITDYLSPDQKEGIFPAKNTLPSGGGAIGYASPNPVEIRDTIGPVEFNNTCC	135	
DB	89	AAVTITDYLSPDQKEGIFPAKNTLPSGGGAIGYASPNPVEIRDTIGPVEFNNTCC	148	
QY	136	RFTSSNNAVNAKIREGGAHAQNLXINHNDVGVGKMFNSYVRGGAISTANTFVSVEN	195	
DB	149	RLFTWRNPYAA-DKIREGGAHAQNLXINHNDVGVGKMFNSYVRGGAISTANTFVSVEN	207	
QY	196	QSCFLFMDNICIQNTAGKGGAIYAGTSNPFESNCDLFFINNACCAGGAIFSPICSLTG	255	
DB	208	QSCFLFMDNICIQNTAGKGGAIYAGTSNPFESNCDLFFINNACCAGGAIFSPICSLTG	267	
QY	256	NRGNIVFYNNRCFKNVEYASSASDGGAIKYTRLDVTGNRGRIFFSNITKNYGGAIYA	315	
DB	268	NRGNIVFYNNRCFKNVEYASSASDGGAIKYTRLDVTGNRGRIFFSNITKNYGGAIYA	327	
QY	316	PVTVLDVNGPTYFINNIANNKGGAIYIDGTSNSKISADRHAIIFENIVTNVNTANGTST	375	
DB	328	PVTVLDVNGPTYFINNIANNKGGAIYIDGTSNSKISADRHAIIFENIVTNVNTANGTST	387	
QY	376	SANPPRRNAITVASSSGEILLGAGSQNLIFYDPIEVSNAGVSFNFKEADQTSVWPSG	435	
DB	388	SANPPRRNAITVASSSGEILLGAGSQNLIFYDPIEVSNAGVSFNFKEADQTSVWPSG	447	
QY	436	ATVNSADFQHNLOKTPAPLTLSNGFLCIEDHAQLTVNRFTQTGGVYSLGNAGVILSCYK	495	
DB	448	ATVNSADFQHNLOKTPAPLTLSNGFLCIEDHAQLTVNRFTQTGGVYSLGNAGVILSCYK	507	
QY	496	NGAGNSASNAITLKHIGLINSILKSGAEIPLWVEPTNNSNNTADTAATFSLSDVKL	555	
DB	508	NGTGDASNASITLKHIGLINSILKSGAEIPLWVEPTNNSNNTADTAATFSLSDVKL	567	
QY	556	SLIDDYGNPSVESTDLTHALSSQPMLSITSEASDNLSDDDMFGLNVPYHGWGLWTWG	615	
DB	568	SLIDDYGNPSVESTDLTHALSSQPMLSITSEASDNLSDDDMFGLNVPYHGWGLWTWG	627	
QY	616	WAKTODPEPASSATITDQKANRPHRTLLLTWLPAGYVPSPKHRSPLIANTLWGNMLLAT	675	
DB	628	WAKTODPEPASSATITDQKANRPHRTLLLTWLPAGYVPSPKHRSPLIANTLWGNMLLAT	687	
QY	676	ESLKNASBELTSDHPFWGITGGGLGMVYQDPRENHPGFHMRSSGYSAGMIAGQTHFTFSL	735	
DB	688	ESLKNASBELTSDHPFWGITGGGLGMVYQDPRENHPGFHMRSSGYSAGMIAGQTHFTFSL	747	
QY	736	KFSQTYTLKLNRYAKNNVSSKNYSCQGEMLFSLQEGFLLTKLVGLYSYGDHNCHEFFYQ	795	
DB	748	KFSQTYTLKLNRYAKNNVSSKNYSCQGEMLFSLQEGFLLTKLVGLYSYGDHNCHEFFYQ	807	
QY	796	ENLTSQGFRTSOTMCGAVFFDLPMKPPFGSTHILTAFFLGAIGYSSLSHFTVEGAYPRSF	855	

DB	808	ENLTSQGFRTSOTMCGAVFFDLPMKPPFGSTHILTAFFLGAIGYSSLSHFTVEGAYPRSF	867	
QY	856	STKTPLINVLVPIGVKGFMAATQRPQAWTVELAQPVLYROEPGIATOLLASKGIWFGS	915	
DB	868	STKTPLINVLVPIGVKGFMAATQRPQAWTVELAQPVLYROEPGIATOLLASKGIWFGS	927	
QY	916	GSPSSRHAMSKISQOTQPLSWLTLHFQYHGFYSSSTFCNYLNGEIALRF	965	
DB	928	GSPSSRHAMSKISQOTQPLSWLTLHFQYHGFYSSSTFCNYLNGEIALRF	977	

RESULT 9
AAE23486
ID AAE23486 standard; Protein; 956 AA.
XX
AC AAE23486;
XX
DT 27-AUG-2002 (first entry)
XX
DE Chlamydia trachomatis L2 PMPE protein #2.
XX
KW Polymorphic membrane protein; PMPE; PMPI; vaccine; trachoma; PID; LGV; urethritis; epididymitis; conjunctivitis; cervicitis; cervical cancer; pelvic inflammatory disease; lymphogranuloma venereum; tubal occlusion; endometritis; salpingitis; inflammation; inflammatory heart disease; cardiomyopathy; infertility; autoimmune myocarditis; atherosclerosis; infection;
KW
KW Chlamydia trachomatis.
OS
XX
XX WO200228998-A2.
XX
PD 11-APR-2002.
XX
PF 28-SEP-2001; 2001WO-US30345.
XX
PR 02-OCT-2000; 2000US-0677752.
XX
PA (ANTE-) ANTEX BIOLOGICS INC.
XX
XX Jackson WJ;
XX
XX WPI; 2002-426107/45.
DR N-PSDB; AAD37835.
DR
PT Novel purified Chlamydia polymorphic membrane protein E or I, useful for preparing vaccines for preventing or treating diseases associated with Chlamydia infection such as trachoma, and infertility -
PT
XX
PS Claim 1; Fig 8; 160pp; English.
XX
CC The invention relates to Chlamydia sp. polymorphic membrane protein (PMP) E and PMPI and nucleic acid molecules encoding such proteins.
CC PMPI and PMPE polypeptides, nucleic acids and vaccines are useful for preventing, treating or ameliorating trachoma, conjunctivitis, tubal occlusion, cervicitis, cervical cancer, pelvic inflammatory disease (PID), lymphogranuloma venereum (LGV), endometritis, epididymitis, salpingitis, infertility, reactive arthritis, inflammatory heart disease, urethritis, autoimmune myocarditis, cardiomyopathy and atherosclerosis. They are also useful as reagents for clinical or medical diagnosis of Chlamydia infections. The present sequence is Chlamydia trachomatis L2 PMPE protein.
CC
XX

Query Match	96.08;	Score 4884;	DB 23;	Length 956;
Best Local Similarity	99.08;	Pred. No. 0;		
Matches 925;	Conservative 5;	Mismatches 4;	Indels 0;	Gaps 0;
QY	32	VPDFTKESLSNKISLTGDTNHLTNCYLDNLRYLAILQKTPNEGAATITDYLGFDTQK	91	
DB	23	VPDFTKESLSNKISLTGDTNHLTNCYLDNLRYLAILQKTPNEGAATITDYLGFDTQK	82	

Qy 92 EGIYFAKNLTPESSGAGIYASNPSTVEIRDTIGVIFENNTCCRPFTSSNPNAAVNKIR 151
Db 83 EGIYFAKNLTPESSGAGIYASNPSTVEIRDTIGVIFENNTCCRPFTSSNPNAAVNKIR 142
Qy 152 EGGATHAQNLYINHNHVDVGFMMKFSYVYRGAIYSTANTFVYSENQSCFLEMDNICIQNT 211
Db 143 EGGATHAQNLYINHNHVDVGFMMKFSYVYRGAIYSTANTFVYSENQSCFLEMDNICIQNT 202
Qy 212 AGKGAIYAGTNSFESNCDLFFINNACCAGGAIFSPICSLTGNRGNIVFYNNRCFKNV 271
Db 203 AGKGAIYAGTNSFESNCDLFFINNACCAGGAIFSPICSLTGNRGNIVFYNNRCFKNV 262
Qy 272 ETASSEASDGGAIKVTRLDVGTNRGRIFFSDNITKNYGGAIYAPVTVLDVNGPTYFINN 331
Db 263 ETASSEASDGGAIKVTRLDVGTNRGRIFFSDNITKNYGGAIYAPVTVLDVNGPTYFINN 322
Qy 332 IANKKGAIYIDGTSNKSISADRAHAIIFENINVTYNANGTSTSANPPRRNAITVASS 391
Db 323 VANKKGAIYIDGTSNKSISADRAHAIIFENINVTYNANGTSTSANPPRRNAITVASS 382
Qy 392 GEILLGAGSSONLIFYDPIEVSNAGVSVPFNKEADOTGVSFSGATVNSADFHORNLOTK 451
Db 383 GEILLGAGSSONLIFYDPIEVSNAGVSVPFNKEADOTGVSFSGATVNSADFHORNLOTK 442
Qy 452 TPAPLTLSNGFLCIEDHAQLTVNRTQTGGVYSLGNGAVLSCYKNGAGNSASNIILKH 511
Db 443 TPAPLTLSNGFLCIEDHAQLTVNRTQTGGVYSLGNGAVLSCYKNGAGNSASNIILKH 502
Qy 512 IGLNLSILKSGAIEPLLWEPPTNNSNYTADTAATFSLDVKLSLIDDDYNSYESTDL 571
Db 503 IGLNLSILKSGAIEPLLWEPPTNNSNYTADTAATFSLDVKLSLIDDDYNSYESTDL 562
Qy 572 THALSSQPMLSISBASDNQLRSDDMDFSGLVNPHVYGOGLTWGAKTQDPEPASSATIT 631
Db 563 THALSSQPMLSISBASDNQLRSDDMDFSGLVNPHVYGOGLTWGAKTQDPEPASSATIT 622
Qy 632 DPQKANFRHRTLLTLWLPAGVVPKHSRPLIANTLGNMMLLATESLKNSAELTPSDHPF 691
Db 623 DPQKANFRHRTLLTLWLPAGVVPKHSRPLIANTLGNMMLLATESLKNSAELTPSDHPF 682
Qy 692 WGITGGGLMMVYQDPRENHPGFMRSRSGYSAGMIAGTHTFSLKFSQTYTKLNERYAKN 751
Db 683 WGITGGGLMMVYQDPRENHPGFMRSRSGYSAGMIAGTHTFSLKFSQTYTKLNERYAKN 742
Qy 752 NVSSKNTSCQEMFLSLQEGFLTKLVGLYSYGDHNCHEFTQGENLTSQGTFRSQTMGG 811
Db 743 NVSSKNTSCQEMFLSLQEGFLTKLVGLYSYGDHNCHEFTQGENLTSQGTFRSQTMGG 802
Qy 812 AVFFDLPMKPGSTHILTAFLGALGIYSSLSHTEVGYAPRSFSTKTPLINLVPIGVK 871
Db 803 AVFFDLPMKPGSTHILTAFLGALGIYSSLSHTEVGYAPRSFSTKTPLINLVPIGVK 862
Qy 872 GSFNNATQPOAWTVELAYQPVLYRQEPGIATQLLASGIWFGSGSPSSRHMSYKISQ 931
Db 863 GSFNNATQPOAWTVELAYQPVLYRQEPGIATQLLASGIWFGSGSPSSRHMSYKISQ 922
Qy 932 TQPLSWLTLHFQYHGFYSSTECNYLNGEIALRF 965
Db 923 TQPLSWLTLHFQYHGFYSSTECNYLNGEIALRF 956

RESULT 10

AAE23472

ID AAE23472 standard; Protein; 500 AA.

XX AC AAE23472;

XX XX

XX XX

XX XX

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XX XX

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XX XX

XX XX

Chlamydia trachomatis L2 PMPE protein fragment #18.

Polymorphic membrane protein; PMPE; PMPI; vaccine; trachoma; PID; LGV; urethritis; epididymitis; conjunctivitis; cervicitis; cervical cancer;

KW pelvic inflammatory disease; lymphogranuloma venereum; tubal occlusion;
KW endometritis; salpingitis; inflammatory heart disease; cardiomyopathy;
KW infertility; autoimmune myocarditis; atherosclerosis; infection;
KW arthritis.
XX Chlamydia trachomatis.
OS WO200228998-A2.
XX 11-APR-2002.
XX 28-SEP-2001; 2001WO-US30345.
XX 02-OCT-2000; 2000US-0677752.
XX (ANTE-) ANTEX BIOLOGICS INC.
XX Jackson WJ;
XX WPI: 2002-426107/45.
XX N-PSDB; AAD37817.
XX Novel purified Chlamydia polymorphic membrane protein E or I, useful
XX for preparing vaccines for preventing or treating diseases associated
XX with Chlamydia infection such as trachoma, and infertility -
XX Claim 8; Page 134-136; 160pp; English.
XX The invention relates to Chlamydia sp. polymorphic membrane protein
XX (PMP) E and PMPI and nucleic acid molecules encoding such proteins.
XX PMPI and PMPE polypeptides, nucleic acids and vaccines are useful for
XX preventing, treating or ameliorating trachoma, conjunctivitis, tubal
XX occlusion, cervicitis, cervical cancer, pelvic inflammatory disease
XX (PID), lymphogranuloma venereum (LGV), endometritis, epididymitis,
XX salpingitis, infertility, reactive arthritis, inflammatory heart
XX disease, urethritis, autoimmune myocarditis, cardiomyopathy and
XX atherosclerosis. They are also useful as reagents for clinical or
XX medical diagnosis of Chlamydia infections. The present sequence is
XX Chlamydia trachomatis L2 PMPE protein fragment.

SQ Sequence 500 AA;

Query Match 51.2%; Score 2605; DB 23; Length 500;

Best Local Similarity 100.0%; Pred. No. 3.1e-185;

Matches 500; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKKAFFFLIGNSLGSLAREVPSRIFLMPNSVPDPTKESLSNKISLTGDTNLTNCYLDN 60

Db 1 MKKAFFFLIGNSLGSLAREVPSRIFLMPNSVPDPTKESLSNKISLTGDTNLTNCYLDN 60

Qy 61 LRYTLAILQKTPNEGAATITDYLSPFDQKEGIYFAKNLTPESSGAGIYASNPSPVEI 120

Db 61 LRYTLAILQKTPNEGAATITDYLSPFDQKEGIYFAKNLTPESSGAGIYASNPSPVEI 120

Qy 121 RDTIGPVIFENNTCCRPFTSSNPNAAVNKIREGGAIIHAQNLYINHNHVDVGFMMKFSYVR 180

Db 121 RDTIGPVIFENNTCCRPFTSSNPNAAVNKIREGGAIIHAQNLYINHNHVDVGFMMKFSYVR 180

Qy 181 GGAISTANTFVYSENQSCFLFMDNICIQTNTAGKGGAIYAGTNSFESNCDLFFINNAC 240

Db 181 GGAISTANTFVYSENQSCFLFMDNICIQTNTAGKGGAIYAGTNSFESNCDLFFINNAC 240

Qy 241 CAGGAIFSPICSLTGNRGNIVFYNNRCFKVETASSASDGGAIKVTRLDVGTNRGRIF 300

Db 241 CAGGAIFSPICSLTGNRGNIVFYNNRCFKVETASSASDGGAIKVTRLDVGTNRGRIF 300

Qy 301 FSDNITKNYGGAIYAPVTVLDVNGPTYFINNIANKGAIYIDGTSNKSISADRAHAIIFN 360

Db 301 FSDNITKNYGGAIYAPVTVLDVNGPTYFINNIANKGAIYIDGTSNKSISADRAHAIIFN 360

Qy 361 ENIVTNTVANGTSTSANPPRRNAITVASSGEILLGAGSSONLIFYDPIEVSNAGVS 420

Db 361 ENIVTNTVANGTSTSANPPRRNAITVASSGEILLGAGSSONLIFYDPIEVSNAGVS 420

QY 421 FNKEADQTSVVFSGATVNSADFHORNLOTKTPAPLTLSNGFLCIEDHAQLTVNRFQTG 480
 Db 421 FNKEADQTSVVFSGATVNSADFHORNLOTKTPAPLTLSNGFLCIEDHAQLTVNRFQTG 480
 QY 481 GVVSLGNGAVLSCYKNGAGN 500
 Db 481 GVVSLGNGAVLSCYKNGAGN 500

RESULT 11

AAV92833
 ID AAY92833 standard; Protein; 931 AA.

AC AAY92833;

XX 29-AUG-2000 (first entry)

XX C. pneumoniae CPN100628 antigen.

XX Antigen; anti-inflammatory; respiratory; antibacterial; anti-asthmatic;
 KW anti-arteriosclerotic; vaccine.

XX Chlamydia pneumoniae.

XX WO200024765-A2.

XX 04-MAY-2000.

XX 28-OCT-1999; 99WO-CA00992.

PR 28-OCT-1998; 98US-0106034.

PR 28-OCT-1998; 98US-0106039.

PR 28-OCT-1998; 98US-0106042.

PR 28-OCT-1998; 98US-0106044.

PR 29-OCT-1998; 98US-0106072.

PR 29-OCT-1998; 98US-0106073.

PR 29-OCT-1998; 98US-0106074.

PR 29-OCT-1998; 98US-0106087.

PR 02-NOV-1998; 98US-0106587.

PR 02-NOV-1998; 98US-0106588.

PR 02-NOV-1998; 98US-0107034.

PR 02-NOV-1998; 98US-0107035.

XX (CONN-) CONNAUGHT LAB LTD.

XX Murdin AD, Oomen RP, Wang J;

XX WPI; 2000-350688/30.

DR N-PSDB; AAA28712, AAA28713.

XX Chlamydia antigens and the proteins they encode, useful for
 PT vaccinating against Chlamydia infections that affect the respiratory
 PT tract

PS Claim 13; Fig 23; 226pp; English.

XX The nucleic acids may be used for the recombinant production of the
 CC Chlamydia polypeptides (either in vivo or in vitro) according to standard
 CC recombinant DNA methodologies. The polypeptides may then be used to
 CC vaccinate against Chlamydia infections in mammals. Chlamydia, such as
 CC C. pneumoniae, are pathogens responsible for upper respiratory tract
 CC infections such as community acquired pneumonia, acute respiratory
 CC disease and bronchitis and may be implicated in atherosclerotic changes
 CC and asthma. The nucleic acids may also be used as probes for detecting
 CC the presence of Chlamydia nucleic acids in samples (and therefore
 CC diagnose infections) and the proteins may be used as antigens for the
 CC production of antibodies that may be used to detect Chlamydia proteins
 CC in samples (e.g. via enzyme linked immunosorbent assay (ELISA)).

XX Sequence 931 AA;

Query Match 22.1%; Score 1123.5; DB 21; Length 931;

Best Local Similarity 30.9%; Pred. No. 1.5e-74;
 Matches 308; Conservative 164; Mismatches 417; Indels 109; Gaps 31;

QY 6 EFELIGNSLGLAREVPSRIFLWPNVSPDPPTKESLNKISLTCGTHNLT-----NC 56

Db 5 FTFVLAN--EGLQLPLETITLSPEYQAAPO-----VGFTHNQDOLAIVGNHD 52

QY 57 YLDNLRYLAILQKTPNEGAATITDYLFFDTQKEGIYFAKNLTPESSGAIGYASPNSP 116

Db 53 FILDYKY-----RSGGALTCKNLL--ISENIGNVFEKNVCPNSGAI-YAAQNC- 101

QY 117 TVEIRDTIGVIPENNTCRPTSSNPNAVNKIRREGGAHQAONLYINIHVDVVGPMKF 176

Db 102 -----TISK--NONYAFITNLVSDNPTATAGSLL--GGALFAINCISITNLGGQTVDNL 152

QY 177 SYVRGGAISTANTFVVSQSCFLFMDNICIOTNTAGKGIYAGVTSNFSNCCDLEFI 236

Db 153 ALNKGALYETNLSIKDNKGPILIKQNRAL--NSDSLGGIYSGNLSNIENSGAIQT 210

QY 237 NNACCAGGAIFS-PICSLTGRNRIYNNRCFKNVETASSEASDGAIAKVTTRLDVTGN 295

Db 211 SNSSGGGGIFSTQTLTITSSNKKLIEISNSAFAN--NYGSNFPNGGGGLTTTFCFILNN 268

QY 296 RGRIFSDNITKNYGAIYAPVTVLDNGPTTFYFINNIANKGAIYID--GTSNKS--ISA 352

Db 269 REGVLFNNSQSGNGAIHAKSIIIIKENGVPVFLNNTATRGGALLNLSAGSNGSPILSA 328

QY 353 DRHAIIFENIVTNTNANGTSTSANPPRRNAITVASSSGEILLGAGSSONLIFYDPIEV 412

Db 329 DNGDIIFNN-----TASKHALNPPYRNAIH-STPNMNIQIGARPYRVLYDPIEH 379

QY 413 S-NAGVSVFNKEADQTSVVFSGATVNSADFHORNLOTKTPAPLTLSNGFLCIEDHAQL 471

Db 380 ELPSSFPILLFETGHTGTVPFSGEYHQNFTDENFFSYLRNTSELROGLAVEDGAGL 439

QY 472 TVNRFTQGGVSLGNGAVLSCYKNGAGN-----SASNAITLKHGLNLSSTLKSQ 523

Db 440 ACYKFFQGGTLLGOGAVITT---AGTPTPSTPTTGVSTITLNHAIIDLPSILSQ 495

QY 524 AEIPLLVETPNNSNYTADTAATFSLSDVKLSLDDYNSPYESTDLTHALSSOPMLSI 583

Db 496 AQAPKIWIYPTKGTSTYEDSNPTIISGT--LTLRNSNEDPYDSLDSHLEKVPLLXI 554

QY 584 SEASDNQLRSDMDPFGSLNV-PHYGQGLWTGWAKTQDPEPASSATITDPQK---ANRF 639

Db 555 VDVAQKINSSQLDLSTLNSGEHYGYQGIWSTYVWET-----TTITNPTSLLGATK 606

QY 640 HRTILLTWLPAGYVPSPKHRSPLIANTLWGNMLLATESLKNSAELTPSDHPFWGITGG-- 697

Db 607 HKLLYANWSPLGYRPHPRRGEFITNALWQSAYTALAGLSLSS-----WDEKGA 658

QY 698 ---GLGMVYODPRENHPGHMRSSGYSAGMIA--GOTHTFSLKFSOTYTKLNERYAKN 751

Db 659 ASLOGIGLLVHOKNGKNGFKGFRSHMTGYSATTEATSSQSPNFSLGFAQFFSKAKHESON 718

QY 752 NVSSKNY---SCQEMFLFSLOEFLTLKLVLG-LYSYGDHNCHEFTYQGENLTSQGTFRSQ 807

Db 719 SFSSHHYFGSMCIAR--YSLQVRILS--VSLAYMFTSEHTTMYQGLLEGNSQGSFHH 774

QY 808 TMGGAVFDLPKMPGSGTHILTAPELGAIGIYSSLSHTEVGAYPRSFSTKPTLINLVLP 867

Db 775 TLAGALSVCFLPQPHGES-LQIYPTITALIRGNLAFAQESGDHAREFSLRPLRDLVSLP 833

QY 868 ICVKGSFNMATOPPAWELAYQVLYRQEPGIATQALLASKGIWFGSCSPSSRAMSVK 927

Db 834 VGIASWKNHHRVPLWLTETSYRSTLYRQDPELHSLKLLISQGTWTQTATPYTNALGIK 893

QY 928 ISQOQTPLSWLFLFOYHGFYSSSTFCNYLNGEIALRF 965

Db 894 VKNTMQVPKVTLSLDYSADISSSTLSHLYLVNVSWMRF 931

RESULT 12

ABB90528	AB B90528 standard; Protein; 938 AA.
XX	AC ABB90528;
XX	DT 29-JUL-2002 (first entry)
XX	DE Chlamydia pneumoniae cp6751 protein, SEQ ID NO:5.
XX	KW Chlamydial infection; antigen; immunogen; vaccine; diagnosis; human respiratory disease; cardiovascular disease; atherosclerosis; coronary artery disease; carotid artery stenosis; myocardial infarction; cerebrovascular disease; aortic aneurysm; claudication; stroke; strain CWL029.
XX	KW Chlamydia pneumoniae.
XX	OS Chlamydia pneumoniae.
XX	FH Key Location/Qualifiers
XX	FT Peptide 1..17
XX	FT FT /label= Signal_peptide
XX	FT Protein 18..938
XX	FT FT /note= "Mature protein"
XX	PN WO200202606-A2.
XX	PD 10-JAN-2002.
XX	PF 03-JUL-2001; 2001WO-IB01445.
XX	PR 03-JUL-2000; 2000GB-0016363.
XX	PR 11-JUL-2000; 2000GB-0017047.
XX	PR 21-JUL-2000; 2000GB-0017983.
XX	PR 07-AUG-2000; 2000GB-0019368.
XX	PR 18-AUG-2000; 2000GB-0020440.
XX	PR 14-SEP-2000; 2000GB-0022583.
XX	PR 10-NOV-2000; 2000GB-0027549.
XX	PR 22-DEC-2000; 2000GB-0031706.
XX	PA (CHIR-) CHIRON SPA.
XX	PI Ratti G, Grandi G;
XX	DR WPI; 2002-154726/20.
XX	DR N-PSDB; ABL91186.
XX	PT Novel Chlamydia pneumoniae protein useful in the manufacture of a medicament for treatment or prevention of infection due to Chlamydia, preferably Chlamydia pneumoniae, and for diagnostic purposes -
XX	PS Claim 1; Page 43; 364pp; English.
XX	CC Sequences ABB90526-ABB90715 represent novel proteins from Chlamydia pneumoniae (strain CWL029), and ABL91184-ABL91373 represent DNA encoding them. The proteins are predicted to be immunogenic and may therefore be useful in vaccine production and for diagnostic purposes. Chlamydia pneumoniae is a common cause of respiratory disease in humans, and is also involved in the development of cardiovascular diseases such as atherosclerosis, coronary artery disease, carotid artery stenosis, myocardial infarction, cerebrovascular disease, aortic aneurysm, claudication and stroke. The proteins and nucleic acids of the invention may be used in vaccines and pharmaceutical compositions for the prevention or treatment of chlamydial infections, particularly Chlamydia pneumoniae infections. The proteins may also be used in the detection of Chlamydia pneumoniae, and the nucleic acids may be used in PCR, branched DNA probe assay or blotting techniques for determining Chlamydia pneumoniae gene expression. The present sequence represents a specifically claimed Chlamydia pneumoniae protein of the invention.
XX	SQ Sequence 938 AA;

Query Match 22.08; Score 1120.5; DB 23; Length 938;
Best Local Similarity 30.9%; Pred. No. 2.5e-74;
Matches 308; Conservative 163; Mismatches 418; Indels 109; Gaps 31;

RESULT 13
AAY35082
ID AAY35082 standard; Protein; 940 AA.

QY 6 E F F L I G N S L G L A R E V P S R I F L M P N S V P D P T K E S L S N K I S L T G D T H N L T -----NC 56
DB 12 F T F V L A N - E G L Q L P L E T I T L S P E Y Q A P Q -----V G F T H N Q N Q D L A I V G N H N D 59
QY 57 Y L D N L R Y I L A I L Q K T P N E G A A V T I D Y L S F F D T Q K E G I Y F A K N L T P E S G G A I G Y A S P N S P 116
DB 60 F I L D Y K Y Y -----R S N G G A L T C K N L L - I S E N I G N V F F E K N V C P N S G G A I - Y A A Q N C - 108
QY 117 T V E I R D T I G P V I F E N N T C C R P F T S S N P N A A V N K I R E G G A I H A Q N L Y I N H N H D V G F M K N F 176
DB 109 -----T I S K - N O N Y A F T T N L V S D N P T A T A G S L L - G G A L F A I N G S I T N N L Q G G T F V D N L 159
QY 177 S Y V R G G A I S T A N T F V V S E N O S C F L F M D N I C I Q T N T A G K G G A I Y A C T S F S E S N N C D L F F I 236
DB 160 A L N K G G A L Y T E T N I S I K D N K G P I I K Q N R A L - N S D S L G G G I Y S N I E N S A I Q I T 217
QY 237 N N A C C A G G A I F S - P I C S L T G N R G N I V F Y N N R C F K N V E T A S S E A S D G G A I K V T T R L D V T G N 295
DB 218 S N S G S G G I F S T Q T L T I S S N K K L I E I S E S A F A N - N Y G S N F N P G G G L T T T F C T I L N N 275
QY 296 R G R I F F S D N I T K Y G G A I Y A P V V I L V D N G P T Y F I N N I A N N K G G A I Y I D - G T S N S K - I S A 352
DB 276 R E G V L F N N Q S Q S N G G A I H A K S I I I K E N G P V Y F L N T A T R G G A L L N L S A G S G N G S F I L S A 335
QY 353 D R H A I I F N E N I V T N V T N A N G T S T A N P P R R N A I T V A S S S G E I L L G A G S S Q N L I F Y D P T E V 412
DB 336 D N G D I I F N N N -----T A S K H A L N P P Y R N A I H - S T P N M N L Q I A R G P Y R V L F Y D P I E H 386
QY 413 S - N A G V S V S F N K E A D Q T G S V V F S G A T V N S A D F H O R N L O T K T P A P L T L S N G F I C I D H A Q L 471
DB 387 E L P S S F P I L F N F E T G H T G T V L F S G E H V H O N F T D E M F F S Y L R N T S E L Q G V L A V E D G A G L 446
QY 472 T V N R F T Q T G G V V S L G N G A V L S C Y K N G A C N -----S A S N A S I T L K H I G N L S I L K S G 523
DB 447 A C Y K F F O R G G T L L L Q G G A V I T T - - - A C T I P T S T P T V G T S T I T L N I A I D L P S I L S F Q 502
QY 524 A E I P L L W V E P T N N S N N Y T A D T A A T F S L S D V K I S L I D D Y G N S P Y E S T D T H A L S S Q P M L S I 583
DB 503 A Q A P K I W I Y P T G T S T Y T E D S N P T I T I S G T - L T L K N S N E D P Y D S L D L S H S L E K V P L L Y I 561
QY 584 S E A S D N Q L R S D D M F S G L N V - P H Y G W Q L T W G A K T O D P E P A S S A T I T D P Q K - - - A N R F 639
DB 562 V D V A A Q K I N S Q L D L S T L N S G E H Y G Y Q I W S T Y W V E T - - - T T I T N P T S L L G A N T K 613
QY 640 H R T L L L T W L P A G Y V P S P K H R S P L A N T L W G N M L L A T E S L K N S A E L T P S D H F W G I T G G - - 697
DB 614 H K L L Y A N M S P L G Y R P H P P E R G E F I T N A L W Q S A Y T A L A G L H S L S - - - W D E E K G H A 665
QY 698 - - - G L G M V Y Q D P R E N H P G F H M R S S G Y S A G M I A - - G O T H T F S L K F S O T Y T K L N E R Y A K N 751
DB 666 A S L O G I G L L V H Q K D K N G F K G F R S H W T G Y S A T E A T S S O S P N F S L G F A G F F K A K E H E S Q N 725
QY 752 N V S S K N Y - - - S C O G E M L F S L O G F L L T K L V G L - Y S Y G D H N C H F Y T Q G E N I T S O G T F R S Q 807
DB 726 S T S S H H V P S G M C I E N T L F - K E W I R L S - - V S L A Y M F T S E H T H T M Y Q L L E G N S Q G S F H N H 781
QY 808 T M G A N V F D L P M K P F G S T H I L T A P L G A L G I Y S S L S H T E V G A Y P R S F S T K T P L I N L V P 867
DB 782 T L A G A L S C V F L P Q P H G E S - L Q I Y P F I T A I R G N L A A F Q E S G D H A R E F S L R H P L T D V S L P 840
QY 868 I G V K S F M A T O R P Q A W T V E L A Y O P V L Y R Q E P G T A T O L L A S K G I W F G S G S P S S R H A M S Y K 927
DB 841 V G I R A S W N H U R V P L V W L T E I S Y S T L Y R Q D P E L H S K L L I S Q G I W T T Q A T P V T Y N A L G I K 900
QY 928 I S Q O T P L S W L T H F Q Y H G F Y S S T F C N Y L N G E I A L R F 965
DB 901 V K N T M Q V P K Y T L S I D Y S A D I S S T L S H Y L A N V A S R M R F 938

XX AC AAY35082;
XX DT 13-SEP-1999 (first entry)
XX DE Chlamydia pneumoniae surface exposed polypeptide.
XX KW Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis;
KW sinusitis; purulent otitis media; erythema nodosum; pharyngitis;
KW vaccine; neutralising epitope.
XX OS Chlamydia pneumoniae.
XX PN WO9927105-A2.
XX PD 03-JUN-1999.
XX PF 20-NOV-1998; 98WO-IB01890.
XX PR 04-NOV-1998; 98US-0107078.
XX PR 21-NOV-1997; 97FR-0014673.
XX PA (GEST) GENSET.
XX PI Griffais R;
XX DR WPI; 1999-357842/30.
XX PT Genome sequence of Chlamydia pneumoniae
XX PS Page 965-967; Disclosure; 1912pp; English.
XX CC AAY34584-y35879 represent the proteins encoded by all the open reading
CC frames in the complete genome (see AAY91990) of Chlamydia pneumoniae.
CC C. pneumoniae causes respiratory disease such as pneumonia and
CC bronchitis and is thought to be a contributing factor in heart
CC disease, sarcoidosis, sinusitis, purulent otitis media, erythema
CC nodosum or pharyngitis. The polypeptides encoded by the open reading
CC frames of the C. pneumoniae genome (see AAY34584-y35879) can be used in
CC immunogenic compositions as vaccines. Vectors containing C. pneumoniae
CC nucleotide sequences can also be used as immunogenic compositions,
CC especially where the vector directs the expression of a neutralising
CC epitope of C. pneumoniae.
XX SQ Sequence 940 AA;
Query Match 22.0%; Score 1120.5; DB 20; Length 940;
Best Local Similarity 30.9%; Pred. No. 2.5e-74;
Matches 308; Conservative 163; Mismatches 418; Indels 109; Gaps 31;
QY 6 FFFLIGSLGLAREVPSRIFLMPNSVPDPPTKESLSNKISLTGDTNLT-----NC 56
DB 14 FFFVLN--EGQLPLETYITLSPEYQAAPQ-----VGFTNQDIAVGNHND 61
QY 57 YLDNLRYILAILQKTPNEGAAYTIDYLSFFDTQKEGIYFAKNLTPESGGAIGAYSPNSP 116
DB 62 FILDYKY-----RNSGALTCRNL--ISENIGNVFEKNCVCPNSGAI-YAQNOC- 110
QY 117 TWEIRDITGVFENNCTCRPTSSNPNAVNKIREGGAHQAQNYIYNHNDVGVGMKNF 176
DB 111 -----TISK--NONYAFNTNVDNPTATAGSL--GGALFAINGSITNLLGGQTFVDNL 161
QY 177 SYVRGGAISTANTFVYVSENOSCFLEMDNICIQTNFAGKGAIACTSNFSFNSNCDLFFI 236
DB 162 ALNKGALYETNLSIKDNKGPILIKQNAL--NSDSGGGIYSGNSLNIEGNSAIIQT 219
QY 237 NNACCAGGAIFS-PICSLTGRNGTIVFYNNRCFKNVETASSPASDGAIKVTRLDVTGN 295
DB 220 SNSGSGGGIFSTQTLTTSNNKLLIESENSAFAN--NYGSNFNPGGGLTTFECTILNN 277
QY 296 RGRIFSDNITKNYGAIYAPVTVLDNCPYFINNIANNKGGAIYID-GTNSK--ISA 352
DB 278 REGVLFNNSQSNGGAIAHAKSIKENGPIYFLNATRGALLNLNLSAGSNGSGFILSA 337

QY 353 DRHAIIFENIVNTNANGTSTSNPPRRNAITVASSGCEILLGAGSSQNLIIFYDPIEV 412
DB 338 DNGDIIFNN-----TASKHALNPPYRNAIH-STPNNNLIQIGARPGYRVLYDPIEH 398
QY 413 S-NAGVSVSFENKEADQTSVVFSGATVNSADPHORNLOTKTPAPLTLNGLFCIEDHAQL 471
DB 389 ELFSSPILFNETGHTGTVLFSGEHVHQNFTDEMNFYSLRNTSELROGLVLADEGAGL 448
QY 472 TVNRFQTQGVVSLGNGAVLSCYKNGAGN-----SASNASITLKHGLNLSLTKSG 523
DB 449 ACYKFFQRCGTLLLGOGAVITT-----AGTIPSPSTPTTVGSTITLHAIIDLPSLSFQ 504
QY 524 AEIPLLWVEPTNNSNNYTADTAATFSLSDVKLSLIDYGNSEYESTDLTHALSSQPMLSI 583
DB 505 AQAPKIWIYPTKTGSTYTEDSNPTITISCT-LTLRNSNEDPYDLDLSHLEKVPLLYI 563
QY 584 SEASDNQLRSDMDDFSGLVN-PHYGQGLWTGWAKTQDPEPASSATITDPOK---ANRP 639
DB 564 VDVAQKINSQDLSTLNSGEHYGYQIWTYVWET-----TTITNPTSLLGANTK 615
QY 640 HRTLLLTWLPAGYVPSPKHRSPLIANTLGNMLLATESLKNSELTPSDHPFWGITGG-- 697
DB 616 HKLLYANWSPLGYRPHPERREGEFITNALWQSAYTALAGLHSLSS-----WDEKGA 667
QY 698 ----GLGMMVYQDPRENHPGFHMRSGYSAGMIA--GQHTFSLKFSQTYTKLNERYAKN 751
DB 668 ASLOGIGLLVHOKDKNGFKGFRSHMTGYSATTEATSSQSPNFSLGFAQFSAKEHESON 727
QY 752 NVSSKNY----SCOGEMFLSLQEGFLTKLVGL-YSGDHCHHFYTOGLENLTSQGTFRSQ 807
DB 728 STSSHFFSGMCIENTLF--KEWIRLS--VSLAYMTSEHTMTYQGLLEGNSQGSFHHN 783
QY 808 TMGGAFFEDLPKMPGSHILTAPELGAIGIYSSLSHTEVGAYPRSFSTKPLINLVLP 867
DB 784 TLAGALSCVFLPDPHGES-LQIYFFITAIIRGNLAQFQESGDHAREFSLHRPLTDVSLP 842
QY 868 ICVKSFMNATQPOAWTVELAYQPVLYROEPGIATQLLASKGIFGSGSPSSRHMSYK 927
DB 843 VGIASWKNHHRVPLVWLTEISYRSTLYQDPELHSLKLLISQGTWTQTATPYTNALGIK 902
QY 928 ISQQTQPLSWLFLHFQYHGFSYSTFCNYLNGEIALRF 965
DB 903 VKNTMQVPKVTLSLDYSADISSSTLSHYLNVAARMRF 940
RESULT 14
AAY35083
ID AAY35083 standard; Protein; 969 AA.
AC AAY35083;
XX 13-SEP-1999 (first entry)
XX Chlamydia pneumoniae surface exposed polypeptide.
DE Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis;
KW sinusitis; purulent otitis media; erythema nodosum; pharyngitis;
KW vaccine; neutralising epitope.
OS Chlamydia pneumoniae.
XX PN WO9927105-A2.
XX PD 03-JUN-1999.
XX 20-NOV-1998; 98WO-IB01890.
XX 04-NOV-1998; 98US-0107078.
XX 21-NOV-1997; 97FR-0014673.
XX (GEST) GENSET.
XX

PI Griffais R;

XX WPI; 1999-357842/30.

XX Genome sequence of Chlamydia pneumoniae

XX Page 967-969; Disclosure; 1912pp; English.

XX AAY34584-Y35879 represent the proteins encoded by all the open reading
 CC frames in the complete genome (see AAY34584-Y35879) of Chlamydia pneumoniae.
 CC C. pneumoniae causes respiratory disease such as pneumonia and
 CC bronchitis and is thought to be a contributing factor in heart
 CC disease, sarcoidosis, sinusitis, purulent otitis media, erythema
 CC nodosum or pharyngitis. The polypeptides encoded by the open reading
 CC frames of the C. pneumoniae genome (see AAY34584-Y35879) can be used in
 CC immunogenic compositions as vaccines. Vectors containing C. pneumoniae
 CC nucleotide sequences can also be used as immunogenic compositions,
 CC especially where the vector directs the expression of a neutralising
 CC epitope of C. pneumoniae.

XX Sequence 969 AA;

Query Match 20.88; Score 1057.5; DB 20; Length 969;
 Best Local Similarity 30.5%; Pred. No. 1.3e-69;
 Matches 302; Conservative 165; Mismatches 447; Indels 77; Gaps 28;

QY 6 FFPLIGNSGLAREVPSRIFLMPNSVDP-----PTKESISLNK-----ISL 46
 Db 25 FLVLGNFTACMGWTFVYSLQTDLSLEKFALEDERFRTSFLDLSLSTLGTGSPITTF 84
 QY 47 TGDPHNLT-NCYLDNRLYLILAILOKTPNEGAATITDYLSPFDQKEGIYFAKNLTPESG 105
 Db 85 VGNRHNSQDVLNSYKSIDNILLWTLSAGAVSCNNFL--LSNVEDHAFSKNLAIGTG 142
 QY 106 GAIGYASPNSTVEIRDTGPIFENNTCCRPFTSSPNPNAVNKIRGGAIHAQ-NLYIN 164
 Db 143 GAIAQCG----ACTITKNRGLPIFFSRGLN-----NASTGGETRGGAACACNGDETIS 191
 QY 165 HNHVDVGFMKNFSVRGGAATSTANTFVSENSCFLFMDNICIQNTAGKGAIGAYAGTSN 224
 Db 192 QNQTFTFVNSVNWGGALSTNGCHRIQSNRAPLLFFN-----NTAPSGGGALRENT 245
 QY 225 SFESNCCDLFFINNACCAGAIFSPI-CSLTGNRGNIIVFYNNRCFKNVTASSEASDGA 283
 Db 246 TISDTRPIVFKNCGNGGAIQISVVAIKNNSGVIFNNNTALSG--SINSGSGGA 303
 QY 284 IKVTRLDVTGNRGRIFFSDNITKNYGGAIYAPVTVLDVNGPTTFINNIANKGAIYID 343
 Db 304 I-YTINLSIDDPGTLIFNNNYCIRDGGAICTQPLTIKNSGHVYFTNN-QGNWGGALMLL 361
 QY 344 GTSNKSISADRHAIIFENIVTNTNANGTSTSANPPRRAITVASSSGEILLGAGSSQN 403
 Db 362 QDSTCLIFAGQNTAFONNEVLTTFG-----RYNAIHTPNS-NQLGANKGYT 410
 QY 404 LIFYDPIEVSNAGVS-VSFNKEADQTSVVFSGATVNSADFQHNRLQTKTPAPLTLSNGF 462
 Db 411 TAFDPDIEHQHPTTNLIFFNPANHQGTILFSSAYIPEASDYENNEFISSKNTSELNGV 470
 QY 463 LCIEDHAQLVNRRTQTGGVVVSLNGAVLSCYKNGAGNSAS-NASITLKHIGLNLSSILK 521
 Db 471 LSIEDRAGWQFYKFTQKGGILKLGHAASIAATTANSETPTSVSGSQVFINNLAINLPSTLA 530
 QY 522 SGAEPILWPEPTNNSNYTADTAFTSLSDVKLSLDDYDGNSPYESTDLTHALSSQPM 581
 Db 531 KG-KAPTLWRPLOSSAPFTNNPTITLSG-PLTLINEENRDPYSDIDSEPLQNTILL 588
 QY 582 SISEASDNQLRSDMDDFSLN-VPHYGQGLWTGWAKTQDPEPASSATITDPOKANRFH 640
 Db 589 SLSDVTARHINTDNFHELSNATEHYGYQIWSYFWET--ITTTNASI---ETANTLY 643
 QY 641 RTLLLTWLPAGYVSPKRPRLPIANTLWGNMLLATESLKNASAEITPSD--HPFWGITGGG 698
 Db 644 RALYANWTPLGYKVNPEYQGLDATTPLWQSFHTWFLSLRSYNRGTGDSDIERPFLFIQIA 703

QY 699 LGMVYODPRENHGPFHMRSSGSYS--AGMIAGQTHTEFSLKFSQTYTKLNERYAKNNYSSK 756
 Db 704 DGLFVHNSIPGAPGFRIQSTIGYSLQASSETSLHOKISLGAQFTRTKELGSSNNVSAH 763
 QY 757 N--YSCQGEMLFSLQEGFLLTKVLGYLSYGDHNCHEFTYQGENLTSCQTFRSTMGGAVF 814
 Db 764 NTVSSLVVELPW-FQEAFAF-ATSTVLAYGYGDHHLHSLHPSHOE-QAECTCYSHTLAAAIG 820
 QY 815 FDLPMKFGSTHITATPLGALGIYSSLSHTEVGAIPRSFSTKTPLINVLVPIGVKGSF 874
 Db 821 CSFPWQOKSYLHL--SPEVQAIAIRSHQTAEEIGDNPKEVSKQPFYNNLTPLGIQGW 878
 QY 875 MNATQRPQAWVELAYQPVLYRQEPGIATOLLASKGIWFGSGSPSSRHMSYKISQQTQP 934
 Db 879 QSKFHVPTWTEWLEUSYEPVLYQQNPQIGVTLASGGSDIILGHNVYRNALGYKVNQTAL 938
 QY 935 LSWLTLHFQYHGFYSSSTFCNLYNGEIALRF 965
 Db 939 FRSLDLFLDYQGSVSSSTSTTHLQAGSTLKF 969

RESULT 15
AAY92832

ID AAY92832 standard; Protein; 1000 AA.

XX AAY92832;

XX AC AAY92832;

XX DT 07-SEP-2000 (first entry)

XX DE C. pneumoniae CPN100626 full-length antigen.

XX DE Antigen; anti-inflammatory; respiratory; antibacterial; anti-asthmatic;

XX DE anti-arteriosclerotic; vaccine.

XX DE Chlamydia pneumoniae.

XX DE WO200024765-A2.

XX PD 04-MAY-2000.

XX PF 28-OCT-1999; 99WO-CA00992.

XX PR 28-OCT-1998; 98US-0106034.

XX PR 28-OCT-1998; 98US-0106039.

XX PR 28-OCT-1998; 98US-0106042.

XX PR 28-OCT-1998; 98US-0106044.

XX PR 29-OCT-1998; 98US-0106072.

XX PR 29-OCT-1998; 98US-0106073.

XX PR 29-OCT-1998; 98US-0106074.

XX PR 29-OCT-1998; 98US-0106087.

XX PR 02-NOV-1998; 98US-0106587.

XX PR 02-NOV-1998; 98US-0106588.

XX PR 02-NOV-1998; 98US-0107034.

XX PR 02-NOV-1998; 98US-0107035.

XX PA (CONN-) CONNAUGHT LAB LTD.

XX PI Murdin AD, Oomen RP, Wang J;

XX DR WPI; 2000-350688/30.

XX DR N-PSDB; AAA28710.

XX PT Chlamydia antigens and the proteins they encode, useful for

XX PT vaccinating against Chlamydia infections that affect the respiratory

XX PS tract

XX PS Claim 13; Fig 21; 226pp; English.

XX CC The nucleic acids may be used for the recombinant production of the
 CC Chlamydia polypeptides (either in vivo or in vitro) according to standard
 CC recombinant DNA methodologies. The polypeptides may then be used to
 CC vaccinate against Chlamydia infections in mammals. Chlamydia, such as

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OM nucleic - nucleic search, using sw model

Run on: February 4, 2003, 15:51:52 ; Search time 543 Seconds

(without alignments)
12018.952 Million cell updates/sec

Title: us-09-677-752-1

Perfect score: 2898

Sequence: 1 atgaaaaagcggttttctt.....aaattgctgcgattcttag 2898

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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2: /SID22/gcgdata/geneseq/geneseq-emb1/NA1981.DAT.*
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4: /SID22/gcgdata/geneseq/geneseq-emb1/NA1983.DAT.*
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6: /SID22/gcgdata/geneseq/geneseq-emb1/NA1985.DAT.*
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23: /SID22/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT.*
24: /SID22/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2898	100.0	2898	24	AAD37798
2	2866	98.9	1038602	20	AAZ01425
3	2821.2	97.3	2895	22	AAH56256
4	2821.2	97.3	2895	24	ABL92485
5	2819.6	97.3	2895	21	AAI64753
6	2777.8	95.9	2934	21	AAA64759
7	2777.8	95.9	2934	22	AAH56262
8	2777.8	95.9	2934	24	ABL92491
9	2776.8	95.8	2871	24	AAD37835

10	1500	51.8	1500	24	AAD37817	Chlamydia trachoma
11	1190.6	41.1	1634	22	AA57011	C. trachomatis DNA
12	321	11.1	321	24	AAD37801	Chlamydia trachoma
13	276	9.5	276	24	AAD37805	Chlamydia trachoma
14	243	8.4	243	24	AAD37802	Chlamydia trachoma
15	228	7.9	228	24	AAD37811	Chlamydia trachoma
16	228	7.9	228	24	AAD37812	Chlamydia trachoma
17	201	6.9	201	24	AAD37804	Chlamydia trachoma
18	198	6.8	198	24	AAD37803	Chlamydia trachoma
19	198	6.8	198	24	AAD37806	Chlamydia trachoma
20	198	6.8	198	24	AAD37808	Chlamydia trachoma
21	183	6.3	183	24	AAD37814	Chlamydia trachoma
22	153	5.3	153	24	AAD37807	Chlamydia trachoma
23	153	5.3	153	24	AAD37815	Chlamydia trachoma
24	136.4	4.7	2805	24	ABL91187	Chlamydia pneumoniae
25	136.4	4.7	273254	21	AA61914	Chlamydia pneumoniae
26	134.8	4.7	1230025	20	AA91990	Nucleotide sequence
27	131.6	4.5	3003	21	AAA28711	C. pneumoniae CPN1
28	131.6	4.5	3200	21	AAA28710	C. pneumoniae CPN1
29	126	4.3	126	24	AAD37800	Chlamydia trachoma
30	115.8	4.0	3092	21	AA50038	DNA encoding Chlam
31	108	3.7	108	24	AAD37809	Chlamydia trachoma
32	108	3.7	108	24	AAD37810	Chlamydia trachoma
33	93	3.2	93	24	AAD37816	Chlamydia trachoma
34	89.6	3.1	2796	21	AAA28713	C. pneumoniae CPN1
35	89.6	3.1	3000	21	AAA28712	C. pneumoniae CPN1
36	88	3.0	2817	24	ABL91186	Chlamydia pneumoniae
37	71.6	2.5	2865	21	AAA28709	C. pneumoniae CPN1
38	71.6	2.5	3150	21	AAA28708	C. pneumoniae CPN1
39	63	2.2	63	24	AAD37813	Chlamydia trachoma
40	48.4	1.7	1511	20	AA60546	Seq ID No: 22 of W
41	48.4	1.7	1515	20	AA60555	C. trachomatis HMW
42	48.4	1.7	2949	21	AA64752	C. trachomatis pmp
43	48.4	1.7	2949	22	AAH56255	Chlamydia trachoma
44	48.4	1.7	2949	24	ABL92484	Chlamydia DNA sequ
45	48.4	1.7	3021	21	AAA64758	C. trachomatis pmp

ALIGNMENTS

RESULT 1

AAD37798
ID AAD37798 standard; DNA; 2898 BP.
XX AAD37798;
AC AAD37798;
XX 27-AUG-2002 (first entry)
XX Chlamydia trachomatis L2 PMPE DNA #1.

XX Polymorphic membrane protein; PMPE; PMPI; vaccine; trachoma; PID; LGV;
XX urethritis; epididymitis; conjunctivitis; cervicitis; cervical cancer;
XX pelvic inflammatory disease; lymphogranuloma venereum; tubal occlusion;
XX endometritis; salpingitis; inflammatory heart disease; cardiomyopathy;
XX infertility; autoimmune myocarditis; atherosclerosis; infection;
XX arthritis; gene; ds.

XX Chlamydia trachomatis.

XX Key Location/Qualifiers

XX CDS 1..2898

XX /*tag= a

XX /product= "Chlamydia trachomatis L2 PMPE protein #1"

XX W0200202898=AA2

XX 11-APR-2002.

XX 28-SEP-2001; 2001WO-US30345.

XX 02-OCT-2000; 2000US-0677752.

XX

Qy	2821	CATTTCAGTATCATGATTCTACTCCTCTCAACCTTCGTAATATCTCAATGGGAA	2880
Db	2821	CATTTCAGTATCATGATTCTACTCCTCTCAACCTTCGTAATATCTCAATGGGAA	2880
Qy	2881	ATTGCTCTGGGATTCTAG	2898
Db	2881	ATTGCTCTGGGATTCTAG	2898
RESULT 2			
AAZ01425			
ID	AAZ01425	standard; DNA; 1038602 BP.	
XX	AAZ01425;		
XX	07-OCT-1999	(first entry)	
XX		Complete genome sequence of Chlamydia trachomatis.	
XX		Vaccine; eye disease; conventional trachoma; nonendemic trachoma;	
KW		paratrachoma; inclusion conjunctivitis; genital disease; perihhepatitis;	
KW		nongonococcal urethritis; epidymitis; cervicitis; salpingitis;	
KW		bartholinitis; pneumopathy; venereal lymphogranulomatosis; ss.	
XX		Chlamydia trachomatis.	
OS			
PN	3692928475-A2.		
XX	10-JUN-1999.		
XX	27-NOV-1998;	98WO-IB01939.	
XX	04-NOV-1998;	98US-0107077.	
PR	28-NOV-1997;	97FR-0015041.	
PR	17-DEC-1997;	97FR-0016034.	
PA	(GEST) GENSET.		
PI	Griffais, R.		
XX	WPI; 1999-371125/31.		
XX		Genome sequence of Chlamydia trachomatis	
PT	Claim 1; Page 373-656;	1755pp; English.	
PS		The present sequence represents the complete genome of Chlamydia	
CC		trachomatis. Open reading frames (ORFs) of the genome encode	
CC		polypeptides AA36754-Y37949. The polypeptides can be used as Vaccines	
CC		agents:Chlamydia trachomatis. Antisense and ribozyme sequences can also	
CC		be used to control growth of the microorganism. Chlamydia trachomatis is	
CC		responsible for a large number of diseases, e.g. eye diseases such as	
CC		conventional trachoma, nonendemic trachoma, paratrachoma, and inclusion	
CC		conjunctivitis; genital diseases such as nongonococcal urethritis,	
CC		epidymitis, cervicitis, salpingitis, perihhepatitis, bartholinitis;	
CC		pneumopathy in breast feeding infants; and venereal	
CC		lymphogranulomatosis. The polypeptides of the invention may be of use in	
CC		treating these diseases.	
XX			
SQ	Sequence 1038602 BP; 304265 A; 214645 C; 214259 G; 305001 T; 432 other;		
	Query Match	98.9%; Score 2866; DB 20; Length 1038602;	
	Best Local Similarity	99.3%; Pred. No. 0;	
	Matches 2878; Conservative	0; Mismatches 20; Indels 0; Gaps	
Qy	1	ATGAAAAAGCGTTTTTCTTTTTCCTTATGGAAATCCCTATCAGGACTAGCTAGAGAG	60
Db	484964	ATGAAAAAGCATCTTTTTTTCCTTATGGAGTCCCTATCAGGACTAGCTAGAGAG	485023
Qy	61	GTTCCTTCTAGATCTTTTTCATATGCCCCAACTCAGTTCCAGATCCTTACGAAAGATCGCTA	120
Db	485024	GTTCCTTCTAGATCTTTTTCATATGCCCCAACTCAGTTCCAGATCCTTACGAAAGATCGCTA	485083

Db 487244 CAAGGAGAAATGCTTCTCATTCATGCAAGAGGTTTCTTGCTGGCTAAATAGTTGGTCTT 487303
QY 2341 TACAGCTATGGACACATACATGTCACCAATTTCTATACCAAGGAGAGAAATCTAACATCT 2400
Db 487304 TACAGCTATGGAGATCAATGTCACCAATTTCTATACCAAGGAGAGAAATCTAACATCT 487363
QY 2401 CAAGGACGTTCCGTTAGTCAAAACGATGGGAGGTGCTGTTTTTTTGGATCCCTATGAAA 2460
Db 487364 CAAGGACGTTCCGTTAGTCAAAACGATGGGAGGTGCTGTTTTTTTGGATCCCTATGAAA 487423
QY 2461 CCCTTTGGATCAACCATATCTACAGCTCCCTTTTGGTGGCTCTGGTATTTATCT 2520
Db 487424 CCCTTTGGATCAACCATATCTACAGCTCCCTTTTGGTGGCTCTGGTATTTATCT 487483
QY 2521 AGCCTGCTCACTTTACTGAGTGGGAGGCTATCCGCAAGCTTTTCTACAAAGACTCCT 2580
Db 487484 AGCCTGCTCACTTTACTGAGTGGGAGGCTATCCGCAAGCTTTTCTACAAAGACTCCT 487543
QY 2581 TTGATCAATGCTCCTAGTCCCTATTGGAGTTAAAGTAGCTTTATGAATGCTACCCAAAGA 2640
Db 487544 TTGATCAATGCTCCTAGTCCCTATTGGAGTTAAAGTAGCTTTATGAATGCTACCCAAAGA 487603
QY 2641 CCTCAAGCCTGACGTGATGATGGCATACCAACCGTTCTGTATAGACAAGACAGGG 2700
Db 487604 CCTCAAGCCTGACGTGATGATGGCATACCAACCGTTCTGTATAGACAAGACAGGG 487663
QY 2701 ATCGGACCCAGCTCCTAGCCAGTAAGGTATTTGGTTGGTAGTGGAGCCCTCATCG 2760
Db 487664 ATCGGACCCAGCTCCTAGCCAGTAAGGTATTTGGTTGGTAGTGGAGCCCTCATCG 487723
QY 2761 GCTCATGCCATGCTCCTATAAAATCTCACAGCAACACACACCTTTTGAGTTGGTTAACTCTC 2820
Db 487724 GCTCATGCCATGCTCCTATAAAATCTCACAGCAACACACACCTTTTGAGTTGGTTAACTCTC 487783
QY 2821 CATTTCCAGTATCATGATTCATCTCCTCTTCAACCTTCTGTAATATCTCAATGGGAA 2880
Db 487784 CATTTCCAGTATCATGATTCATCTCCTCTTCAACCTTCTGTAATATCTCAATGGGAA 487843
QY 2881 ATTGCTCTGCGATTCTAG 2898
Db 487844 ATTGCTCTGCGATTCTAG 487861

RESULT 3
AAH56256
ID AAH56256 standard; DNA; 2895 BP.
XX
AC AAH56256;
XX
DT 05-SEP-2001 (first entry)
XX
DE Chlamydia trachomatis pmpE gene.
XX
KW Chlamydia; vaccine; infection; fusion protein; antigen;
KW pelvic inflammatory disease; trachoma; atherosclerosis; heart disease;
KW acute respiratory tract infection; Cap1; CF529; OMCB;
KW polymorphic membrane protein; pmp; thiol specific antioxidant; TSA; ds.
OS Chlamydia trachomatis.
XX
PN WO200140474-A2.
XX
PD 07-JUN-2001.
XX
PF 04-DEC-2000; 2000WO-US32919.
XX
PR 03-DEC-1999; 99US-0454684.
PR 19-APR-2000; 2000US-0556877.
PR 20-JUN-2000; 2000US-0598419.
XX
PA (CORI-) CORIXA CORP.
XX
PI Probst P, Bhatia A, Skeiky YAW, Fling SP, Scholler J;

XX WPI; 2001-374831/39.
XX
DR Chlamydia polypeptides and fusion proteins useful for preventing pelvic
PT inflammatory disease, trachoma, acute respiratory tract infections,
PT atherosclerosis and heart disease -
XX
PS Claim 1; Page 181-182; 295pp; English.
XX
CC The present nucleotide sequence is provided in a specification
CC relating to compounds and methods for the treatment and diagnosis of
CC chlamydial infection. The compounds provided include polypeptides and
CC fusion proteins comprising immunogenic portions of Chlamydia antigens
CC and DNA sequences encoding such polypeptides. They are useful for
CC vaccinating against chlamydial infection, which causes pelvic
CC inflammatory disease, trachoma, acute respiratory tract infections,
CC atherosclerosis and heart disease.
XX
SQ Sequence 2895 BP; 866 A; 632 C; 558 G; 839 T; 0 other;

Query Match 97.3%; Score 2821.2; DB 22; Length 2895;
Best Local Similarity 98.6%; Pred. No. 0;
Matches 2857; Conservative 0; Mismatches 38; Indels 3; Gaps 1;
QY 1 ATGAAAAAGCGTTTCTTTTCTTATGGAACCTCCCTATCAGGACTAGCTAGAGAG 60
Db 1 ATGAAAAAGCGTTTCTTTTCTTATGGAACCTCCCTATCAGGACTAGCTAGAGAG 60
QY 61 GTTCCTTCTAGAACTTTCTTATGCCAACTCAGTCCAGATCCCTACGAAAGAGTCGCTA 120
Db 61 GTTCCTTCTAGAACTTTCTTATGCCAACTCAGTCCAGATCCCTACGAAAGAGTCGCTA 120
QY 121 TCAATAAATAGTTTTCACAGGACACTCACAATCTCACTAAGTCTGCTATCGATAAC 180
Db 121 TCAATAAATAGTTTTCACAGGACACTCACAATCTCACTAAGTCTGCTATCGATAAC 180
QY 181 CTACGCTACATCTGGCTTATCTACAAAACTCCCAATGAAGGAGTCTGTCAATA 240
Db 181 CTACGCTACATCTGGCTTATCTACAAAACTCCCAATGAAGGAGTCTGTCAATA 240
QY 241 ACAGATTACCTAAGCTTTTGTGATACAAAAAGAGTATTTATTTGCAAAAAATCTC 300
Db 241 ACAGATTACCTAAGCTTTTGTGATACAAAAAGAGTATTTATTTGCAAAAAATCTC 300
QY 301 ACCCTGAAAGTGTGGTGGCTTATGCGAGTCCCAATTCCTACCGTGAGATT 360
Db 301 ACCCTGAAAGTGTGGTGGCTTATGCGAGTCCCAATTCCTACCGTGAGATT 360
QY 361 CGTGATACAATAGTCCCTGTAATCTTTGAAAAATATCTTTGAGAGACCATTTACATCG 420
Db 361 CGTGATACAATAGTCCCTGTAATCTTTGAAAAATATCTTTGAGAGACCATTTACATCG 420
QY 421 AGTATCTAATGAGCTGTTTAAATAAGAGAGCGGAGCCATTCATGCTCAAAAT 480
Db 421 AGAATCTTATGCTGCTG---ATAAATAAGAGAGCGGAGCCATTCATGCTCAAAAT 477
QY 481 CTTTACATAAATCATAATCATGATGTCGATTTATGAAGAACTTTCTTATGTCGA 540
Db 478 CTTTACATAAATCATAATCATGATGTCGATTTATGAAGAACTTTCTTATGTCGA 537
QY 541 GGAGGAGCCATTAGTACCGCTAAATACCTTTTGTGTGAGCGAGATCAGCTTTGTTCTC 600
Db 538 GGAGGAGCCATTAGTACCGCTAAATACCTTTTGTGTGAGCGAGATCAGCTTTGTTCTC 597
QY 601 TTTATGGACAACATCTGTATTCAAACTAATACAGCAGGAAAGGTGGCGCTATCTATGCT 660
Db 598 TTTATGGACAACATCTGTATTCAAACTAATACAGCAGGAAAGGTGGCGCTATCTATGCT 657
QY 661 GGAACGAGCAATCTTTTGTGAGTAAATACCTGCGATCTCTTTTATCAATAAGCCCTGT 720
Db 658 GGAACGAGCAATCTTTTGTGAGTAAATACCTGCGATCTCTTTTATCAATAAGCCCTGT 717
QY 721 TGTGAGGAGGAGGAGATCTTCTCCCTATCTTCTTCTTAACAGGAAATCGTGGTAAACATC 780

Db 718 TGTGAGGAGGAGATCTCTCCCTATCTGTCTCTAAGAGAAATCGTGTAAATC 777
QY 781 GTTTTCTATTAACAAATCGCTCTTAAAAATGTAGAACAGCTTCTCAGAGCTTCTGAT 840
Db 778 GTTTTCTATTAACAAATCGCTCTTAAAAATGTAGAACAGCTTCTCAGAGCTTCTGAT 837
QY 841 GGAGGAGCAATTAAGTAATCTACTCGCTAGATGTTACAGGCAATCGTGTAGATCTTT 900
Db 838 GGAGGAGCAATTAAGTAATCTACTCGCTAGATGTTACAGGCAATCGTGTAGATCTTT 897
QY 901 TTTAGTGACAATATCAAAAAATATAGGGGAGCTATTTACGGTCTCTGTAGTTACCTA 960
Db 898 TTTAGTGACAATATCAAAAAATATAGGGGAGCTATTTACGGTCTCTGTAGTTACCTA 957
QY 961 GTGGATAATGGCCCTACTACTTATAAACAATATGCCAATATAGGGGGGCGGTATC 1020
Db 958 GTGGATAATGGCCCTACTACTTATAAACAATATGCCAATATAGGGGGGCGGTATC 1017
QY 1021 TATATAGACGAAACCAAGCACTCCAAAATTTCTGCCAGCGCATGCTATTTTAAAT 1080
Db 1018 TATATAGACGAAACCAAGCACTCCAAAATTTCTGCCAGCGCATGCTATTTTAAAT 1077
QY 1081 GAAATATTTGTGACTAATGTAACTAATGAAATGGTACAGTACGTACGTAAATCTCCT 1140
Db 1078 GAAATATTTGTGACTAATGTAACTAATGAAATGGTACAGTACGTACGTAAATCTCCT 1137
QY 1141 AGAAGAAATCAATACAGTACAGTACCTCTCTGGTGAATTTCTATTAGGAGCAGGAGT 1200
Db 1138 AGAAGAAATCAATACAGTACAGTACCTCTCTGGTGAATTTCTATTAGGAGCAGGAGT 1197
QY 1201 AGCCAAAATTTAATTTTATGATCTCTATTGAAGTTAGCAATGCAGGGTCTCTGTCTC 1260
Db 1198 AGCCAAAATTTAATTTTATGATCTCTATTGAAGTTAGCAATGCAGGGTCTCTGTCTC 1257
QY 1261 TTCAATAAGGAAGCTGATCAACAGGCTCTGTAGTATTTTCAGGAGCTACTGTTAAATCT 1320
Db 1258 TTCAATAAGGAAGCTGATCAACAGGCTCTGTAGTATTTTCAGGAGCTACTGTTAAATCT 1317
QY 1321 GCAGATTTTCAATCAAGCAATTTACAAACAAACACCTGCACCCCTTACTCTCAGTAAT 1380
Db 1318 GCAGATTTTCAATCAAGCAATTTACAAACAAACACCTGCACCCCTTACTCTCAGTAAT 1377
QY 1381 GGTTCCTATGTATCGAAGATCATGCTCAGCTTACAGTGAATCGATTACACAACTGGG 1440
Db 1378 GGTTCCTATGTATCGAAGATCATGCTCAGCTTACAGTGAATCGATTACACAACTGGG 1437
QY 1441 GGTGTTGTTCTCTGGGAATGAGCAGTTCGTAGTTGCTATAAAAATGGTGCAGGAAT 1500
Db 1438 GGTGTTGTTCTCTGGGAATGAGCAGTTCGTAGTTGCTATAAAAATGGTGCAGGAGAT 1497
QY 1501 TCTGCTAGCAATGCTCTATACACTGAAGCATATTTGGATTGAATCTTCTTCCATCTG 1560
Db 1498 TCTGCTAGCAATGCTCTATACACTGAAGCATATTTGGATTGAATCTTCTTCCATCTG 1557
QY 1561 AAAAGTGGTCTGAGATTCCTTTATTTGGGTAGAGCTACAAATACAGCAATAACTAT 1620
Db 1558 AAAAGTGGTCTGAGATTCCTTTATTTGGGTAGAGCTACAAATACAGCAATAACTAT 1617
QY 1621 ACAGCAGATCTACGACTACCTTTTTCATTAAGTGTATGTAAGTCTCAGTCAATGTAGAC 1680
Db 1618 ACAGCAGATCTACGACTACCTTTTTCATTAAGTGTATGTAAGTCTCAGTCAATGTAGAC 1677
QY 1681 TATGGGAATTCCTTTATGAATCCAGATCTAACCCATGCTGTGATCAAGCCATG 1740
Db 1678 TATGGGAATTCCTTTATGAATCCAGATCTAACCCATGCTGTGATCAAGCCATG 1737
QY 1741 CTATCTATTTCTGAGGCTAGTGATACCAAGTAAAGTCTGATGATGATTTTTCGGGA 1800
Db 1738 CTATCTATTTCTGAGGCTAGTGATACCAAGTAAAGTCTGATGATGATTTTTCGGGA 1797
QY 1801 CTAAATGTCCTCTATTTAGTGGCAAGGACTTTGGACTTTGGGCTGGGCAAAACTCAA 1860
|||||

Db 1798 CTAAATGTCCTCTCATTTATGATGGCAAGGACTTTTGGACTTTGGGCTGGGCAAAACTCAA 1857
QY 1861 GATCCAGAACACGATCTTTCAGCAACAATCAGATGCCAACAAGCAATAGATTTCCAT 1920
Db 1858 GATCCAGAACACGATCTTTCAGCAACAATCAGATGCCAACAAGCAATAGATTTCCAT 1917
QY 1921 AGAACCTTATTTACTGACTTGGCTTCCCTGCTGGGTATGTTCTAGCCCCAACAAGT 1980
Db 1918 AGAACCTTATTTACTGACTTGGCTTCCCTGCTGGGTATGTTCTAGCCCCAACAAGT 1977
QY 1981 CCCTCATAGCAATACCTTATGGGGAATATGCTGCTGCCAACAGAACTTTAAAAAT 2040
Db 1978 CCCTCATAGCTAACCTTATGGGGAATATGCTGCTGCCAACAAGCTTTAAAAAT 2037
QY 2041 AGTGCAGAACTGACACCTAGTATCATCTTCTGGGGAATTTACAGGAGGAGTACG 2100
Db 2038 AGTGCAGAACTGACACCTAGTATCATCTTCTGGGGAATTTACAGGAGGAGTACG 2097
QY 2101 ATGATGGTTTACCAAGATCCTCGAGAAATCATCTCGATTTCCATATGCGCTCTCCGGA 2160
Db 2098 ATGATGGTTTACCAAGATCCTCGAGAAATCATCTCGATTTCCATATGCGCTCTCCGGA 2157
QY 2161 TACTCTCGGGGATGATAGCAGGCGCAGACACACCTTCTCATTTGAAATTTCACTCAGC 2220
Db 2158 TACTCTCGGGGATGATAGCAGGCGCAGACACACCTTCTCATTTGAAATTTCACTCAGC 2217
QY 2221 TACACAAACTCAATGAGCTTACGCAAAAACAGATATCTTCTAAAAATTTACTCATGC 2280
Db 2218 TACACAAACTCAATGAGCTTACGCAAAAACAGATATCTTCTAAAAATTTACTCATGC 2277
QY 2281 CAAGGAGAAATGCTCTTCTCATTTGCAAGAAAGTTTCTGCTGACTAAATTTAGTTGGCT 2340
Db 2278 CAAGGAGAAATGCTCTTCTCATTTGCAAGAAAGTTTCTGCTGACTAAATTTAGTTGGCT 2337
QY 2341 TACAGCTATGAGAGCAATAACTGTACCAATTTCTATACCAAGAGAGAAATCTAACATCT 2400
Db 2338 TACAGCTATGAGAGCAATAACTGTACCAATTTCTATACTCAAGGAGAGAAATCTAACATCT 2397
QY 2401 CAAGGAGCTTCCGTAGTCAACGATGGGAGTGCTGTTTTTTTTTGTATCTCCCTATGAAA 2460
Db 2398 CAAGGAGCTTCCGTAGTCAACGATGGGAGTGCTGTTTTTTTTTGTATCTCCCTATGAAA 2457
QY 2461 CCCTTGGATCAACGCAATATCTGACAGCTCCCTTTTTTAGTGCTCTTGGTATTTATCT 2520
Db 2458 CCCTTGGATCAACGCAATATCTGACAGCTCCCTTTTTTAGTGCTCTTGGTATTTATCT 2517
QY 2521 AGCTGTCTCAGTCTTACTGAGTGGGAGCTATCCGGAAGCTTTTCTACAAAGACTCCT 2580
Db 2518 AGCTGTCTCAGTCTTACTGAGTGGGAGCTATCCGGAAGCTTTTCTACAAAGACTCCT 2577
QY 2581 TTGATCAATGCTCTAGTCCCTATTGGAGTTAAAGTAGCTTTATGAATGCTACCCAAAGA 2640
Db 2578 TTGATCAATGCTCTAGTCCCTATTGGAGTTAAAGTAGCTTTATGAATGCTACCCACAGA 2637
QY 2641 CCTCAAGCTTGGACTAGAAATTTGGCATACCAACCGGTTCTGTATAGACAAGAACAGGG 2700
Db 2638 CCTCAAGCTTGGACTAGAAATTTGGCATACCAACCGGTTCTGTATAGACAAGAACAGGG 2697
QY 2701 ATCGGACCCAGCTCTCAGCAGTAAGGGTATTTGGTGGTAGTGAAGCCCTCATCG 2760
Db 2698 ATCGGACCCAGCTCTCAGCAGTAAGGGTATTTGGTGGTAGTGAAGCCCTCATCG 2757
QY 2761 CGTCATGCCATGCTCTATAAATCTCACAGCAACAACTTTGAGTTGGTTAACTCTC 2820
Db 2758 CGTCATGCCATGCTCTATAAATCTCACAGCAACAACTTTGAGTTGGTTAACTCTC 2817
QY 2821 CATTTCCAGTATCATGGATTTACTCTCTTCAACCTTCTGTAAATTTCTCAATGGGAA 2880
Db 2818 CATTTCCAGTATCATGGATTTACTCTCTTCAACCTTCTGTAAATTTCTCAATGGGAA 2877
QY 2881 ATTTGCTCTCGATTTCTAG 2898
Db 2878 ATTTGCTCTCGATTTCTAG 2895

Db 1318 GCAGATTTTCATCAACGCAATTTACAAACAAAACACCTGCACCCCTTACTCTCAGTAAT 1377
QY 1381 GGTTCCTATGATCGAAGATCATGCTCAGCTTACAGTGAATCGATTACACAACTGGG 1440
Db 1378 GGTTCCTATGATCGAAGATCATGCTCAGCTTACAGTGAATCGATTACACAACTGGG 1437
QY 1441 GGTGTTCTTCTCTCTGGGAATGGAGCAGTTCTGAGTTGCTATAAAATGTTGTCAGGAAAT 1500
Db 1438 GGTGTTGTTTCTCTGGGAATGGAGCAGTTCTGAGTTGCTATAAAATGTTGTCAGGAGAT 1497
QY 1501 TCTGCTAGCAATGCCTCTATAACACGATGAAGCATATTGGATTGAATCTTCTTCCATTCTG 1560
Db 1498 TCTGCTAGCAATGCCCTATAACACGATGAAGCATATTGGATTGAATCTTCTTCCATTCTG 1557
QY 1561 AAAAGTGGTCTGAGATTCCTTATTGTTGGGTAGAGCCTACAAAATAACAGCAATAACTAT 1620
Db 1558 AAAAGTGGTCTGAGATTCCTTATTGTTGGGTAGAGCCTACAAAATAACAGCAATAACTAT 1617
QY 1621 ACAGCAGATCTCAGCTACCTTTTTCATTAAAGTGATGTAAAACCTCTCAGCTATTGATGAC 1680
Db 1618 ACAGCAGATCTCAGCTACCTTTTTCATTAAAGTGATGTAAAACCTCTCAGCTATTGATGAC 1677
QY 1681 TATGGGAATTCCTTATGAATCCACAGATCTAAACCATGCTCTGTGATCAGAGCCTATG 1740
Db 1678 TAGGGGAACCTCTCTTATGAATCCACAGATCTGACCCATGCTCTGATCAGAGCCTATG 1737
QY 1741 CTATCTATTCTTGAGGCTAGTGATAACACAGCTAAAGTATGATATGATTTTTCGGGA 1800
Db 1738 CTATCTATTCTTGAGGCTAGTGATAACACAGCTAAAGTATGATATGATTTTTCGGGA 1797
QY 1801 CTAAATGTCCTTCATTTATGATGGCAAGACCTTTGGACCTGGGGTGGGCAAAAACCTAA 1860
Db 1798 CTAAATGTCCTTCATTTATGATGGCAAGACCTTTGGACCTGGGGTGGGCAAAAACCTAA 1857
QY 1861 GATCCAGAACCCAGCATCTTCAGCAACAATCACAGATCCCAAAAAGCCCAATAGATTCCAT 1920
Db 1858 GATCCAGAACCCAGCATCTTCAGCAACAATCACAGATCCCAAAAAGCCCAATAGATTCCAT 1917
QY 1921 AGAACCTTATTAAGTGGCTTCTGCTGGGTATGTTCTTCCAGCAAGCAAGT 1980
Db 1918 AGAACCTTATTAAGTGGCTTCTGCTGGGTATGTTCTTCCAGCAAGCAAGT 1977
QY 1981 CCCCTCATAGCAATACCTTATGGGGATATGCTGCTGCAACAGAAAGCTTAAAAAT 2040
Db 1978 CCCCTCATAGCTTAACACCTTATGGGGATATGCTGCTGCAACAGAAAGCTTAAAAAT 2037
QY 2041 AGTCAGAACTGACACCTAGTATCATCTTTCTGGGAATACAGAGGAGGACTAGGC 2100
Db 2038 AGTCAGAGCTGACACCTAGTATCATCTTTCTGGGNAATACAGAGGAGGACTAGGC 2097
QY 2101 ATGATGGTTTACCAAGATCCTCGAGAAATCATCTGGATGCCATATGCTCTTCCGGA 2160
Db 2098 ATGATGGTTTACCAAGATCCTCGAGAAATCATCTGGATGCCATATGCTCTTCCGGA 2157
QY 2161 TACTCTCGGGGATCATAGCAGGCGAGACACACCTTCTCATTTGAAATTCAGTCAGAC 2220
Db 2158 TACTCTCGGGGATCATAGCAGGCGAGACACACCTTCTCATTTGAAATTCAGTCAGAC 2217
QY 2221 TACACCAAACTCAATGAGCGTTTACGCAAAAACACAGTATCTTCTAAAAAATTAATCTATGC 2280
Db 2218 TACACCAAACTCAATGAGCGTTTACGCAAAAACACAGTATCTTCTAAAAAATTAATCTATGC 2277
QY 2281 CAAGGAGAAATGCTCTTCTCATTTGCAAGAGTTTCTGCTGACTTAAATTAATGTTGGGCTT 2340
Db 2278 CAAGGAGAAATGCTCTTCTCATTTGCAAGAGTTTCTGCTGACTTAAATTAATGTTGGGCTT 2337
QY 2341 TACAGCTATGAGACCACTAATCTGTCACCATTTCTATATCCCAAGGAGAAATCTAACATCT 2400
Db 2338 TACAGCTATGAGACCACTAATCTGTCACCATTTCTATATCAAGGAGAAATCTAACATCT 2397
QY 2401 CAAGGAGCTTCCGCTAGTCAACAGATGGGAGTGTCTTTTTTTTGTATCTCCCTATGAAA 2460
|||||

Db 2398 CAAGGAGCTTCCGCACTCAACGATGGAGGTCTCTCTTTTTTGATCTCCCTATGAAA 2457
QY 2461 CCCTTTGGATCAAGCATATACTGACAGCTCCCTTTTTTAGTGCTCTTTGGTATTTATCT 2520
Db 2458 CCCTTTGGATCAAGCATATACTGACAGCTCCCTTTTTTAGTGCTCTTTGGTATTTATCT 2517
QY 2521 AGCTGTCTCAGTTTACTGAGGTGGAGCCTATCCGGAAGCTTTTCTACAAAGACTCCT 2580
Db 2518 AGCTGTCTCAGTTTACTGAGGTGGAGCCTATCCGGAAGCTTTTCTACAAAGACTCCT 2577
QY 2581 TTGATCAATCTCCTAGTCCCTATTGGAGTTAAAGGTAGCTTTATGAATGCTACCAAGA 2640
Db 2578 TTGATCAATCTCCTAGTCCCTATTGGAGTTAAAGGTAGCTTTATGAATGCTACCAAGA 2637
QY 2641 CCTCAAGCCCTGGAGCTGTAGAAATTTGGCATACAAACCCCTCTGTATAGACAAAGAACCAAGG 2700
Db 2638 CCTCAAGCCCTGGAGCTGTAGAAATTTGGCATACAAACCCCTCTGTATAGACAAAGAACCAAGG 2697
QY 2701 ATCGGACCCAGCTCCTAGCCAGTAAGGTAATTTGGTTTGGTAGTGAAGCCCTCATCG 2760
Db 2698 ATCGGACCCAGCTCCTAGCCAGTAAGGTAATTTGGTTTGGTAGTGAAGCCCTCATCG 2757
QY 2761 CGTCATGCCATGTCCTATAAAATCTCACAGCAACACACCTTTGAGTTGTTAACTCTC 2820
Db 2758 CGTCATGCCATGTCCTATAAAATCTCACAGCAACACACCTTTGAGTTGTTAACTCTC 2817
QY 2821 CATTTCCAGTATCATGGATTCTACTCTTCAACCTTCTGTAATATCTCAATGGGAA 2880
Db 2818 CATTTCCAGTATCATGGATTCTACTCTTCAACCTTCTGTAATATCTCAATGGGAA 2877
QY 2881 ATGCTCTCGGATTCTAG 2898
Db 2878 ATGCTCTCGGATTCTAG 2895
RESULT 5
AAA64753
ID AAA64753 standard; DNA; 2895 BP.
XX
AC AAA64753;
XX
DT 02-FEB-2001 (first entry)
XX
DE C. trachomatis pmpE gene coding sequence.
XX
KW Chlamydial infection; sexually transmitted disease;
KW pelvic inflammatory disease; PID; tubal obstruction; infertility;
KW trachoma; blindness; acute respiratory tract infection;
KW atherosclerosis; coronary heart disease; antibacterial; ss.
XX
OS Chlamydia trachomatis.
XX
PN WO200034483-A2.
XX
PD 15-JUN-2000.
XX
PF 08-DEC-1999; 99WO-US29012.
XX
PR 08-DEC-1998; 98US-0208277.
XX
PR 08-APR-1999; 99US-0288594.
XX
PR 01-OCT-1999; 99US-0410568.
XX
PR 22-OCT-1999; 99US-0426571.
XX
PA (CORI-) CORIXA CORP.
XX
PI Probst P, Bhatia A, Skeiky YAW, Fling SP, Jen S, Stromberg EJ;
XX
XX WPI; 2000-431303/37.
XX
PT Isolated polypeptide for diagnosis and treatment of Chlamydia infection
XX comprises immunogenic portion of Chlamydia antigen, which comprises
XX amino acid sequence encoded by polynucleotide sequence -

Claim 1; Pages 173-174; 256pp; English.

The present invention relates to new nucleic acid sequences and the proteins encoded by the nucleic acid sequences. The encoded proteins comprise an immunogenic portion of a Chlamydia antigen. The encoded proteins are useful for the serodiagnosis and treatment of Chlamydia infection. Chlamidiae are intracellular bacterial pathogens that are responsible for a wide variety of human infections. *C. trachomatis* infection is one of the most common sexually transmitted diseases and can lead to pelvic inflammatory disease (PID), resulting in tubal obstruction and infertility. Trachoma due to ocular infection with *C. trachomatis* is the leading cause of preventable blindness worldwide. *C. pneumoniae* is a major cause of acute respiratory tract infections in humans and is also thought to play a role in the pathogenesis of atherosclerosis and coronary heart disease. The present sequence is a nucleic acid sequence isolated in the present invention.

Sequence 2895 BP; 866 A; 633 C; 558 G; 838 T; 0 other;

Query Match 97.3%; Score 2819.6; DB 21; Length 2895;
Best Local Similarity 98.6%; Pred. No. 0;
Matches 2856; Conservative 0; Mismatches 39; Indels 3; Gaps 1;

QY	1	ATGAAAAAGCGTTTTTCTTTTCCCTTATTTGGAACCTCCTATCAGGACTAGCTAGAGAG	60
Db	1	ATGAAAAAGCGTTTTTCTTTTCCCTTATCGGAAACTCCCTATCAGGACTAGCTAGAGAG	60
QY	61	GTTCCTCTAGAATCTTTCTATATGCCCACTCAGTTCAGATCCTACGAAAGTCGCTTA	120
Db	61	GTTCCTCTAGAATCTTTCTATATGCCCACTCAGTTCAGATCCTACGAAAGTCGCTTA	120
QY	121	TCAATATAAAATAGTTTGACAGGAGACACTCAAACTCACTAACCTGCTATCTCGATAAC	180
Db	121	TCAATATAAAATAGTTTGACAGGAGACACTCAAACTCACTAACCTGCTATCTCGATAAC	180
QY	181	CTACGCTACATACTGGCTATTTCTACAAAAAATCCCAATGAAGAGCTGCTGTCACAATA	240
Db	181	CTACGCTACATACTGGCTATTTCTACAAAAAATCCCAATGAAGAGCTGCTGTCACAATA	240
QY	241	ACAGATTACCTAAGCTTTTTTGATACACAAAAAAGAGGTATTTATTTTGCAAAAAATCTC	300
Db	241	ACAGATTACCTAAGCTTTTTTGATACACAAAAAAGAGGTATTTATTTTGCAAAAAATCC	300
QY	301	ACCCCTGAAAGTGGTGGGATGGTATCGAGTCCCAATTCCTACCGTGGAGATT	360
Db	301	ACCCCTGAAAGTGGTGGGATGGTATCGAGTCCCAATTCCTACCGTGGAGATT	360
QY	361	CGTGATACAATAGTCTCTGTAATCTTTGAAAATAATACTTGTGAGAGCACTTACATCG	420
Db	361	CGTGATACAATAGTCTCTGTAATCTTTGAAAATAATACTTGTGAGAGCACTTACATCG	420
QY	421	AGTAATCCTAATGCAGCTGTTAATAAATAAGAGAGCGGAGCCATTTCATGCTCAAAAT	480
Db	421	AGAAATCCTTATGCTGCG--ATAAATAAGAGAGCGGAGCCATTTCATGCTCAAAAT	477
QY	481	CTTTACATAAATCATTAATCATGATGGTGGATTTATGAAGAACTTTTCTTATGTCGA	540
Db	478	CTTTACATAAATCATTAATCATGATGGTGGATTTATGAAGAACTTTTCTTATGTCGAA	537
QY	541	GGAGGAGCCATTAGTACCGCTAATACCTTTGTTGTGAGCGAGAAATCAGTCTTTCTTC	600
Db	538	GGAGGAGCCATTAGTACCGCTAATACCTTTGTTGTGAGCGAGAAATCAGTCTTTCTTC	597
QY	601	TTTATGGACAACATCTGTATTCAAACTAATACAGAGGAAAGGTGGCGCTATCTATGCT	660
Db	598	TTTATGGACAACATCTGTATTCAAACTAATACAGAGGAAAGGTGGCGCTATCTATGCT	657
QY	661	GGACGAGCAATTTCTTTGAGAGTAATAACTGCGATCTCTCTTTATCAATAACGCGCTG	720
Db	658	GGAACGAGCAATTTCTTTGAGAGTAATAACTGCGATCTCTCTTCATCAATAACGCGCTG	717
QY	721	TGTGCAGGAGGAGCATCTTCTCCCGTATCTGTCTTCTAACAGGAATCGTGGTAACATC	780

QY 1861 GATCCAGAACGACGATCTTACGCAACAATCACAGATCCACAAAAAGCAATAGATTCCAT 1920
Db 1858 GATCCAGAACGACGATCTTACGCAACAATCACAGATCCACAAAAAGCAATAGATTCCAT 1917
QY 1921 AGAACCTTATCTAGCTTGGCTTCCCTGCTGGGTATGTTCTAGCCGCAACAGAGAT 1980
Db 1918 AGAACCTTATCTAGCTTGGCTTCCCTGCTGGGTATGTTCTAGCCGCAACAGAGAT 1977
QY 1981 CCCCTATAGCAATACCTTATGGGGAATATGCTGCTGCAACAGAAAGCTTAAAAAT 2040
Db 1978 CCCCTATAGCAATACCTTATGGGGAATATGCTGCTGCAACAGAAAGCTTAAAAAT 2037
QY 2041 AGTGCAGAACTGACACCTAGTATGATTCCTTCTGGGAAATTACAGGAGGAGACTAGGC 2100
Db 2038 AGTGCAGAGCTGACACCTAGTATGATTCCTTCTGGGAAATTACAGGAGGAGACTAGGC 2097
QY 2101 ATGATGGTTTACCAAGATCTTCGAGAAATCATCTGGATTCATATGCGCTCTTCGGA 2160
Db 2098 ATGATGGTTTACCAAGATCTTCGAGAAATCATCTGGATTCATATGCGCTCTTCGGA 2157
QY 2161 TACTCTCGGGGATGATAGCAGGCGACACACACCTTCTCATTGAAATTCAGTCAGACC 2220
Db 2158 TACTCTCGGGGATGATAGCAGGCGACACACACCTTCTCATTGAAATTCAGTCAGACC 2217
QY 2221 TACACAACTCAATGAGCGTTACGCAAAAAACAGCTATCTTCTAAAAATTACTCATGC 2280
Db 2218 TACACAACTCAATGAGCGTTACGCAAAAAACAGCTATCTTCTAAAAATTACTCATGC 2277
QY 2281 CAAGGAGAAATGCTCTCTCATTTGCAAGAGGTTTCTGCTGACTAAATAGTTGGGCTT 2340
Db 2278 CAAGGAGAAATGCTCTCTCATTTGCAAGAGGTTTCTGCTGACTAAATAGTTGGGCTT 2337
QY 2341 TACAGCTATGGAGACCAATACCTGACCAATTTCTATACCAAGGAGAAATCTAACATCT 2400
Db 2338 TACAGCTATGGAGACCAATACCTGACCAATTTCTATACCAAGGAGAAATCTAACATCT 2397
QY 2401 CAAGGAGCGTTGCGTAGTCAAGAGTGGAGGTCGTTTTTTTGGATCTCCCTATGAAA 2460
Db 2398 CAAGGAGCGTTGCGTAGTCAAGAGTGGAGGTCGTTTTTTTGGATCTCCCTATGAAA 2457
QY 2461 CCCTTTGGATCAACGATATCTGACAGCTCCCTTTTATAGTGCTCTGGTATTATCT 2520
Db 2458 CCCTTTGGATCAACGATATCTGACAGCTCCCTTTTATAGTGCTCTGGTATTATCT 2517
QY 2521 AGCTGTCTCACTTTACTGAGTGGAGGCTATCCGCGAAGCTTTTCTACAAGACTCCT 2580
Db 2518 AGCTGTCTCACTTTACTGAGTGGAGGCTATCCGCGAAGCTTTTCTACAAGACTCCT 2577
QY 2581 TTGATCAATGCTCTAGTCCCTATTCGAGTTAAGGTAGCTTTTATGATCTACCCAAAGA 2640
Db 2578 TTGATCAATGCTCTAGTCCCTATTCGAGTTAAGGTAGCTTTTATGATCTACCCAAAGA 2637
QY 2641 CCTAAGCCTGAGCTGTAGAAATGGCATACCAACCGTTCTGTATAGACAAGAACAGG 2700
Db 2638 CCTAAGCCTGAGCTGTAGAAATGGCATACCAACCGTTCTGTATAGACAAGAACAGG 2697
QY 2701 ATCGGACCCAGCTCTAGCCAGTAAAGGTATTTGGTTGGTGAAGCCCTCATCG 2760
Db 2698 ATCGGACCCAGCTCTAGCCAGTAAAGGTATTTGGTTGGTGAAGCCCTCATCG 2757
QY 2761 CGTCATGCCATGCTCTATATAAATCTCACAGCAACACACCTTTGAGTTGGTTAACTCTC 2820
Db 2758 CGTCATGCCATGCTCTATATAAATCTCACAGCAACACACCTTTGAGTTGGTTAACTCTC 2817
QY 2821 CATTTCCAGTATCATGGATTCTTACTCCCTTCAACCTTCTGTAAATATCTCAATGGGAA 2880
Db 2818 CATTTCCAGTATCATGGATTCTTACTCCCTTCAACCTTCTGTAAATATCTCAATGGGAA 2877
QY 2881 ATTGCTCTGGGATTCAG 2898
Db 2878 ATTGCTCTGGGATTCAG 2895

RESULT 6

AAA64759
ID AAA64759 standard; DNA; 2934 BP.
XX
AC
XX AAA64759;
DT 02-FEB-2001 (first entry)
XX
DE C. trachomatis pmpE gene coding sequence minus the signal sequence.
XX
KW Chlamydial infection; sexually transmitted disease;
KW pelvic inflammatory disease; PID; tubal obstruction; infertility;
KW trachoma; blindness; acute respiratory tract infection;
KW atherosclerosis; coronary heart disease; antibacterial; ss.
XX
OS Chlamydia trachomatis.
XX
PN W0200034483-A2.
XX
PD 15-JUN-2000.
XX
PF 08-DEC-1999; 99WO-US29012.
XX
PR 08-DEC-1998; 98US-0208277.
PR 08-APR-1999; 99US-0288594.
PR 01-OCT-1999; 99US-0410568.
PR 22-OCT-1999; 99US-0426571.
XX
PA (CORI-) CORIXA CORP.
XX
PI Probst P, Bhatia A, Skeiky YAW, Fling SP, Jen S, Stromberg EJ;
XX
XX WPI; 2000-431303/37.
XX
PT Isolated polypeptide for diagnosis and treatment of Chlamydia infection
PT comprises immunogenic portion of Chlamydia antigen, which comprises
XX amino acid sequence encoded by polynucleotide sequence -
XX
PS Claim 1; Pages 200-201; 256pp; English.
XX
CC The present invention relates to new nucleic acid sequences and the
CC proteins encoded by the nucleic acid sequences. The encoded proteins
CC comprise an immunogenic portion of a Chlamydia antigen. The encoded
CC proteins are useful for the serodiagnosis and treatment of Chlamydia
CC infection. Chlamydiae are intracellular bacterial pathogens that are
CC responsible for a wide variety of human infections. C. trachomatis
CC infection is one of the most common sexually transmitted diseases and can
CC lead to pelvic inflammatory disease (PID), resulting in tubal obstruction
CC and infertility. Trachoma due to ocular infection with C. trachomatis is
CC the leading cause of preventable blindness worldwide. C. pneumonia is a
CC major cause of acute respiratory tract infections in humans and is also
CC thought to play a role in the pathogenesis of atherosclerosis and
CC coronary heart disease. The present invention is a nucleic acid sequence
XX isolated in the present invention.

Sequence 2934 BP; 875 A; 645 C; 575 G; 839 T; 0 other;

Query Match 95.9%; Score 2777.8; DB 21; Length 2934;
Best Local Similarity 98.6%; Pred. No. 0;
Matches 2813; Conservative 0; Mismatches 37; Indels 3; Gaps 1;
QY 46 GGACTAGCTAGAGAGTTCCTTCTAGAAATCTTCTATGCCCACTCAGTTCACATCCT 105
Db 85 GGACTAGCTAGAGAGTTCCTTCTAGAAATCTTCTATGCCCACTCAGTTCACATCCT 144
QY 106 ACGAAGAGTCCGTATCAATAAATAGTTTGACAGGAGACACTCACAATCTCACTAAC 165
Db 145 ACGAAGAGTCCGTATCAATAAATAGTTTGACAGGAGACACTCACAATCTCACTAAC 204
QY 166 TCGTATCTCGATAACCTACGTACATACCTATGCTATTTACAAAAAACHTCCCAATGAAGA 225
Db 205 TCGTATCTCGATAACCTACGTACATACCTATGCTATTTTACAAAAAACHTCCCAATGAAGA 264

Qy	226	GCTGCTGTCACAATAACAGATTACCTTAAGCTTTTGTGATACACAAAAAGAGGTATTAT	285
Db	265	GCTGCTGTCAACAATAACAGATTACCTTAAGCTTTTGTGATACACAAAAAGAGGTATTAT	324
Qy	286	TTTGCAAAAAATCTCACCCCTGAAAGTGGTGGGATGGTATGCGAGTCCCAATTCCT	345
Db	325	TTTGCAAAAAATCTCACCCCTGAAAGTGGTGGGATGGTATGCGAGTCCCAATTCCT	384
Qy	346	CCTACCGTGGAGATTCGTGATACAATPAGTGCCTGTAATCTTTGAAAAATAACTTGTGTC	405
Db	385	CCTACCGTGGAGATTCGTGATACAATPAGTGCCTGTAATCTTTGAAAAATAACTTGTGTC	444
Qy	406	AGACCAATTATCATCGAGTAATCCTAATGCAGCTGTTAATAAAATAGAGAGCGGAGCC	465
Db	445	AGACTATTTACATGGAGAAATCCTTATGCTGGT--ATAAAATAGAGAGCGGAGCC	501
Qy	466	ATTCAATGCTCAAAATCTTTACATPAAATCATAATCATGATGGTCCGAGTTTATGAAGAAC	525
Db	502	ATTCAATGCTCAAAATCTTTACATPAAATCATAATCATGATGGTCCGAGTTTATGAAGAAC	561
Qy	526	TTTTCATTATGCTCGAGAGGAGGCCATTAGTACGGCTAATACCTTTGTTGTCGAGGAGAAT	585
Db	562	TTTTCATTATGCTCAAGGAGAGGCCATTAGTACGGCTAATACCTTTGTTGTCGAGGAGAAT	621
Qy	586	CAGTCTTGTGTTTCTCTTTATGGACAACATCTGTATTCAAACCTAATACAGCAGGAAAGGT	645
Db	622	CAGTCTTGTGTTTCTCTTTATGGACAACATCTGTATTCAAACCTAATACAGCAGGAAAGGT	681
Qy	646	GGCGCTATCTATGCTGGAAGAGCAATCTTTTGGAGAGTAATAACTGCGATCTCTCTTT	705
Db	682	GGCGCTATCTATGCTGGAAGAGCAATCTTTTGGAGAGTAATAACTGCGATCTCTCTTC	741
Qy	706	ATCAATAACGCCTTGTTGTCGAGAGAGGATCTTCTCCCTATCTGTTCTCTACAGGA	765
Db	742	ATCAATAACGCCTTGTTGTCGAGAGAGGATCTTCTCCCTATCTGTTCTCTACAGGA	801
Qy	766	AATCGTGGTAACATCGTTTCTTATACAATCGCTGCTTTAAAAATGTAGAAACAGCTTCT	825
Db	802	AATCGTGGTAACATCGTTTCTTATACAATCGCTGCTTTAAAAATGTAGAAACAGCTTCT	861
Qy	826	TCAGAAAGCTTCTGATGGAGAGCAATTAAGTAACCTACTCGCCTAGATGTTACAGGCAAT	885
Db	862	TCAGAAAGCTTCTGATGGAGAGCAATTAAGTAACCTACTCGCCTAGATGTTACAGGCAAT	921
Qy	886	CGTGGTAGGATCTTTTTTAGTGACAATATCAAAAAAATTATGCGGAGACTATTACGCT	945
Db	922	CGTGGTAGGATCTTTTTTAGTGACAATATCAAAAAAATTATGCGGAGACTATTACGCT	981
Qy	946	CCTGTAGTACCCCTAGTGGATATGGCCCTACTCTTATATAACAATATCGCCAAATAAT	1005
Db	982	CCTGTAGTACCCCTAGTGGATATGGCCCTACTCTTATATAACAATATCGCCAAATAAT	1041
Qy	1006	AAGGGGGCGCTATCTATATAGACGGAACCGACAATCCAAAAATTTCTGCCGACCGCAT	1065
Db	1042	AAGGGGGCGCTATCTATATAGACGGAACCGACAATCCAAAAATTTCTGCCGACCGCAT	1101
Qy	1066	GCTATATATTTTAAATGAAAATATTGTGACTAATGTAACCTAATGCNAATGGTACCAGTACG	1125
Db	1102	GCTATATATTTTAAATGAAAATATTGTGACTAATGTAACCTAATGCNAATGGTACCAGTACG	1161
Qy	1126	TCAGCTAATCCTCCTAGAGAAATGCAATTAACAGTAGCAAGCTCCTCTGGTGAATTCCTA	1185
Db	1162	TCAGCTAATCCTCCTAGAGAAATGCAATTAACAGTAGCAAGCTCCTCTGGTGAATTCCTA	1221
Qy	1186	TTAGGACGAGGAGTAGCCAAAATTTAATTTTTTATGATCCTATTGAAGTTTAGCAATGCA	1245
Db	1222	TTAGGACGAGGAGTAGCCAAAATTTAATTTTTTATGATCCTATTGAAGTTTAGCAATGCA	1281
Qy	1246	GGGCTCTCTGTGCTTCAATAGGAGCTGATCAACAGGCTCTGTAGTATTTTCAGGA	1305
Db	1282	GGGCTCTCTGTGCTTCAATAGGAGCTGATCAACAGGCTCTGTAGTATTTTCAGGA	1341

Qy	1306	GCTACTGTTAAATTCTCGAGATTTTCATCAACGCCAATTTTACAACAACAAAACACCTGCACCC	1365
Db	1342	GCTACTGTTAAATTCTCGAGATTTTCATCAACGCCAATTTTACAACAACAAAACACCTGCACCC	1401
Qy	1366	CTTACTCTCAGTAATAATGGTTTTCTATGTATCTGAAGATCATGCTCACGTTACAGTGAATCGA	1425
Db	1402	CTTACTCTCAGTAATAATGGTTTTCTATGTATCTGAAGATCATGCTCACGTTACAGTGAATCGA	1461
Qy	1426	TTCACAAAACTGGGGTGTTGTTCTCTTGGGAATGGAGCAGTTTCTGAGTTGCTATAAA	1485
Db	1462	TTCACAAAACTGGGGTGTTGTTCTCTTGGGAATGGAGCAGTTTCTGAGTTGCTATAAA	1521
Qy	1486	AATGGTCGAGAAATTC TGCTAGCAATGCC TCTATAACACTGAACCATATTTGGATTGAAT	1545
Db	1522	AATGGTCAGGAGATTCTGCTAGCAATGCC TCTATAACACTGAACCATATTTGGATTGAAT	1581
Qy	1546	CTTTCTTCCAATCTGAAAAAGTGGTGCTGAGATTCCTTTATTTGGGTAGAGCCTACAAT	1605
Db	1582	CTTTCTTCCAATCTGAAAAAGTGGTGCTGAGATTCCTTTATTTGGGTAGAGCCTACAAT	1641
Qy	1606	AACAGCAATAACTATACGACAGATCTCGAGCTACTCTTTTCATTAAGTGATGTAACACTC	1665
Db	1642	AACAGCAATAACTATACGACAGATCTCGAGCTACTCTTTTCATTAAGTGATGTAACACTC	1701
Qy	1666	TCACTCAATTGATGACTATGGGAATTCCTCTTATGAATCCACAGATCTAACCCATGCTCTG	1725
Db	1702	TCACTCAATTGATGACTACGGGAACCTCCCTTATGAATCCACAGATCTGACCATGCTCTG	1761
Qy	1726	TCATCACAGCCTATGCTATCTATTTCTGAGGCTAGTGATACACGCTAAGATCTGATGAT	1785
Db	1762	TCATCACAGCCTATGCTATCTATTTCTGAGGCTAGTGATACACGCTAAGATCTGATGAT	1821
Qy	1786	ATGGAATTTTTCGGGACTAAATGTCCTCATTTATGGATGGCAAGACTTTGGACTTGGGGC	1845
Db	1822	ATGGAATTTTTCGGGACTAAATGTCCTCATTTATGGATGGCAAGACTTTGGACTTGGGGC	1881
Qy	1846	TGGGCAAAAACCTCAAGATCAGAACAGCATCTTCAGCAACAATCACAGATCCACA AAAA	1905
Db	1882	TGGGCAAAAACCTCAAGATCAGAACAGCATCTTCAGCAACAATCACATGATCCACA AAAA	1941
Qy	1906	GCCAAATAGATTCATAGAACCCTTATTACTGACTTGGCTTCGTCGCGGTATGTTCTTAGC	1965
Db	1942	GCCAAATAGATTCATAGAACCCTTACTACTAATGCTTCCTGCGGGATGTTCCCTAGC	2001
Qy	1966	CCGAAACACAGAAAGTCCCCTCATAGCGAATACCTTATGGGGAATATGCTGCTTGC AACA	2025
Db	2002	CCAAACACAGAAAGTCCCCTCATAGCTAACACCTTATGGGGAATATGCTGCTTGC AACA	2061
Qy	2026	GAAGCTTAAAAAATAGTCGAACTGACACCTAGTGATFATPCPTTCTGGGGAATTACA	2085
Db	2062	GAAGCTTAAAAAATAGTCGAGAGCTGACACCTAGTGGTCTATCCCTTCTGGGGAATTACA	2121
Qy	2086	GGAGGAGGACTAGGCATGATGGTTTTACCAAGATCCTCGAGAAAATCATCCTTGGATTCCAT	2145
Db	2122	GGAGGAGGACTAGGCATGATGGTTTTACCAAGATCCTCGAGAAAATCATCCTTGGATTCCAT	2181
Qy	2146	ATGGGCTCTTCCGGATAC TCTGGGGGATGATAGCAGGGCAGACACACCTTCTCATTTG	2205
Db	2182	ATGGGCTCTTCCGGATAC TCTGGGGGATGATAGCAGGGCAGACACACCTTCTCATTTG	2241
Qy	2206	AAATTCAGTCAGACCTACACCAAACCTCAATAGCGTTTACGCAAAAAAACAGTATCTTCT	2265
Db	2242	AAATTCAGTCAGACCTACACCAAACCTCAATAGCGTTTACGCAAAAAAACAGTATCTTCT	2301
Qy	2266	AAAAATTTACTGCGCAAGGAGAAATGCTTCTCATTTGCAAGAAGGTTTCTTCTGCTGACT	2325
Db	2302	AAAAATTTACTGCGCAAGGAGAAATGCTTCTCATTTGCAAGAAGGTTTCTTCTGCTGACT	2361
Qy	2326	AAATTAGTTGGGCTTTACAGCTATGGAGACCATAACTGTCACCATTTCTATACCCAAGGA	2385
Db	2362	AAATTAGTTGGGCTTTACAGCTATGGAGACCATAACTGTCACCATTTCTATACCCAAGGA	2421
Qy	2386	GAAATCTAAACATCTCAAGGGAGCTTCCGCTAGTCAAAAGCATGGGAGTGCTGTTTTTTTTT	2445

Db 2422 GAAATCTTACATCTCAAGGACGTTCCGCACTCAAAACGATGGAGTCTGCTCTTTT 2481
Qy 2446 GATCTCCCTATGAACCCCTTGGATCAACGCATATACTACAGCTCCCTTTTATAGTGCT 2505
Db 2482 GATCTCCCTATGAACCCCTTGGATCAACGCATATACTACAGCTCCCTTTTATAGTGCT 2541
Qy 2506 CTTGGTATTATTCTAGCCTGCTCACTTTACTAGGTTGGGAGCCTATCCGGAAGCTTT 2565
Db 2542 CTTGGTATTATTCTAGCCTGCTCACTTTACTAGGTTGGGAGCCTATCCGGAAGCTTT 2601
Qy 2566 TCTACAAAGACCTCTTGTATCAATGCTAGTCCCTATTTGGAGTTAAAGTAGCTTTATG 2625
Db 2602 TCTACAAAGACCTCTTGTATCAATGCTAGTCCCTATTTGGAGTTAAAGTAGCTTTATG 2661
Qy 2626 AATGCTACCAAGACCTCAAGCCTGGAGCTGTAGAAATGGCATACCAACCCCTCTGTAT 2685
Db 2662 AATGCTACCAAGACCTCAAGCCTGGAGCTGTAGAAATGGCATACCAACCCCTCTGTAT 2721
Qy 2686 AGACAAGAACAGGATCCGACCCAGCTCCCTAGCCAGTAAGGTTATTTGGTTGGTAGT 2745
Db 2722 AGACAAGAACAGGATCCGACCCAGCTCCCTAGCCAGTAAGGTTATTTGGTTGGTAGT 2781
Qy 2746 GGAAGCCCTCATCGGTCATCGCATGCTCCTATATAAAATCTCACAGCAACAACTTTG 2805
Db 2782 GGAAGCCCTCATCGGTCATCGCATGCTCCTATATAAAATCTCACAGCAACAACTTTG 2841
Qy 2806 AGTTGGTTAACTCTCCATTTCCAGTATCATGATCTACTCTCTTCAACCTTCTGTAT 2865
Db 2842 AGTTGGTTAACTCTCCATTTCCAGTATCATGATCTACTCTCTTCAACCTTCTGTAT 2901
Qy 2866 TATCTCAATGGGAAATGCTCTCGGATTTCTAG 2898
Db 2902 TATCTCAATGGGAAATGCTCTCGGATTTCTAG 2934

RESULT 7

AAH56262
ID AAH56262 standard; DNA; 2934 BP.
XX
AC AAH56262;
XX
DT 05-SEP-2001 (first entry)
XX
DE Chlamydia trachomatis pmpE gene.
XX
KW Chlamydia; vaccine; infection; fusion protein; antigen;
KW pelvic inflammatory disease; trachoma; atherosclerosis; heart disease;
KW acute respiratory tract infection; Cap1; CF529; OMCB;
KW polymorphic membrane protein; pmp; thiol specific antioxidant; TSA; ds.
XX
OS Chlamydia trachomatis.
XX
PN W0200140474-A2.
XX
PD 07-JUN-2001.
XX
PF 04-DEC-2000; 2000WO-US32919.
XX
PR 03-DEC-1999; 99US-0454684.
PR 19-APR-2000; 2000US-0556877.
PR 20-JUN-2000; 2000US-0598419.
XX
PA (CORI-) CORIXA CORP.
XX
PI Probst P, Bhatia A, Skelky YAW, Fling SP, Scholler J;
XX
DR WPI; 2001-374831/39.
XX
PT Chlamydia polypeptides and fusion proteins useful for preventing pelvic
PT inflammatory disease, trachoma, acute respiratory tract infections,
PT atherosclerosis and heart disease -
XX

PS Claim 1; Page 207; 295pp; English.
XX
CC The present nucleotide sequence is provided in a specification
CC relating to compounds and methods for the treatment and diagnosis of
CC chlamydial infection. The compounds provided include polypeptides and
CC fusion proteins comprising immunogenic portions of Chlamydia antigens
CC and DNA sequences encoding such polypeptides. They are useful for
CC vaccinating against chlamydial infection, which causes pelvic
CC inflammatory disease, trachoma, acute respiratory tract infections,
CC atherosclerosis and heart disease.
XX
SQ Sequence 2934 BP; 875 A; 645 C; 575 G; 839 T; 0 other;
Query Match 95.9%; Score 2777.8; DB 22; Length 2934;
Best Local Similarity 98.6%; Pred. No. 0;
Matches 2813; Conservative 0; Mismatches 37; Indels 3; Gaps 1;
Qy 46 GGACTAGCTAGAGAGGTTCCCTTCTAGAAATCTTTTATGCCCAACTCAGTTCAGATCCT 105
Db 85 GGACTAGCTAGAGAGGTTCCCTTCTAGAAATCTTTTATGCCCAACTCAGTTCAGATCCT 144
Qy 106 AGAAGAGTCCCTATCAAAATAAATAGTTTGGAGGAGACACTCACAAATCTCACTAAC 165
Db 145 AGAAGAGTCCCTATCAAAATAAATAGTTTGGAGGAGACACTCACAAATCTCACTAAC 204
Qy 166 TGCTATCTCGATAAACCCTACGCTACATACCTATTCTACAAAAAACTCCCAATGAAGA 225
Db 205 TGCTATCTCGATAAACCCTACGCTACATACCTATTCTACAAAAAACTCCCAATGAAGA 264
Qy 226 GCTGCTGCACAAATACAGATTACCTAAGCTTTTGTGATACAAAAAAGAGGTATTTAT 285
Db 265 GCTGCTGCACAAATACAGATTACCTAAGCTTTTGTGATACAAAAAAGAGGTATTTAT 324
Qy 286 TTTGCAAAAAATCTCACCCCTGAAAGTGGTGGGATTTATCCGAGTCCCAATTCCT 345
Db 325 TTTGCAAAAAATCTCACCCCTGAAAGTGGTGGGATTTATCCGAGTCCCAATTCCT 384
Qy 346 CCTACCGTGGAGATTCGGTATACAAATAGTCTCTTAATCTTTGAAAAATAACTTGTTCG 405
Db 385 CCTACCGTGGAGATTCGGTATACAAATAGTCTCTTAATCTTTGAAAAATAACTTGTTCG 444
Qy 406 AGACCATTTACATCGAGTAATCCTTAATCGAGCTGTTAATAAATAGAGAGCGGAGGCC 465
Db 445 AGACTATTTTACATCGAGTAATCCTTAATCGAGCTGTTAATAAATAGAGAGCGGAGGCC 501
Qy 466 ATTCAATGCTCAAAATCTTTACATAATCATATGATGTCGGATTTTATGAGAAC 525
Db 502 ATTCAATGCTCAAAATCTTTACATAATCATATGATGTCGGATTTTATGAGAAC 561
Qy 526 TTTTCTTATGTCGAGGAGGCCATTAGTACCCTAATACCTTTTGTGTGAGCGAGAT 585
Db 562 TTTTCTTATGTCGAGGAGGCCATTAGTACCCTAATACCTTTTGTGTGAGCGAGAT 621
Qy 586 CAGTCTGTTTCTCTTTATGGACAACATCTGTATTAACACTTAATACAGCAGGAAAGGT 645
Db 622 CAGTCTGTTTCTCTTTATGGACAACATCTGTATTAACACTTAATACAGCAGGAAAGGT 681
Qy 646 GCGCTATCTATGCTGGAACGAGCAATTTTGGAGCTAATAACTGCGATCTCTTCTTT 705
Db 682 GCGCTATCTATGCTGGAACGAGCAATTTTGGAGCTAATAACTGCGATCTCTTCTTTC 741
Qy 706 ATCAATAACGCTGTTGTCAGGAGGAGGATCTTCTCCCTATCTGTTCTCTAACAGGA 765
Db 742 ATCAATAACGCTGTTGTCAGGAGGAGGATCTTCTCCCTATCTGTTCTCTAACAGGA 801
Qy 766 AATCGTGTAAATCGTTTCTTATTAACAATCGCTCTTTTAAAAATGTAGAAACAGCTTCT 825
Db 802 AATCGTGTAAATCGTTTCTTATTAACAATCGCTCTTTTAAAAATGTAGAAACAGCTTCT 861
Qy 826 TCAGAGCTTCTGATGGAGGAGCAATTAAGTAACTACTCCGCTAGATGTTACAGGCAAT 885
Db 862 TCAGAGCTTCTGATGGAGGAGCAATTAAGTAACTACTCCGCTAGATGTTACAGGCAAT 921

QY 886 CGTGGTAGGATCTTTTGTAGTGAACAATATACAAAAAATATATGCGGAGCTATTTACGCT 945
DB 922 CGTGGTAGGATCTTTTGTAGTGAACAATATACAAAAAATATATGCGGAGCTATTTACGCT 981
QY 946 CCTGTAGTACCCCTAGTGGATAATGGCCCTACCTTCTATATAACAATATCGCCAATAAT 1005
DB 982 CCTGTAGTACCCCTAGTGGATAATGGCCCTACCTTCTATATAACAATATCGCCAATAAT 1041
QY 1006 AAGGGGGCGCTATCTATATAGAGGGAACCAAGCAACTCCAAAATTTCTGCCGACCGGCAT 1065
DB 1042 AAGGGGGCGCTATCTATATAGAGGGAACCAAGCAACTCCAAAATTTCTGCCGACCGGCAT 1101
QY 1066 GCTATATTTTAAAGAAATATTTGTGACTAATGTAAGTAAATGAAATGTTGACGACG 1125
DB 1102 GCTATATTTTAAAGAAATATTTGTGACTAATGTAAGTAAATGTTGACGACG 1161
QY 1126 TCAGCTAATCTCTAGAGAAATGCAATACAGTACGAGCTCTCTGGTGAATCTTA 1185
DB 1162 TCAGCTAATCTCTAGAGAAATGCAATACAGTACGAGCTCTCTGGTGAATCTTA 1221
QY 1186 TTAGGAGCAGGAGTAGCCAAAATTTAATTTTATGATCCTATTGAAGTTAGCAATGCA 1245
DB 1222 TTAGGAGCAGGAGTAGCCAAAATTTAATTTTATGATCCTATTGAAGTTAGCAATGCA 1281
QY 1246 GGGGTCTGTGCTTCAATAAGAAAGCTGATCAAAAGGCTCTGTAGTATTTTCAGGA 1305
DB 1282 GGGGTCTGTGCTTCAATAAGAAAGCTGATCAAAAGGCTCTGTAGTATTTTCAGGA 1341
QY 1306 GCTACTGTTAATCTGCAGATTTTCATCAAGCGAATTTACAAACAAAACACCTGCGACC 1365
DB 1342 GCTACTGTTAATCTGCAGATTTTCATCAAGCGAATTTACAAACAAAACACCTGCGACC 1401
QY 1366 CTTACTCTCAGTAATGTTTCTATGATGGAAGATCATGCTCAGCTTACAGTGAATCGA 1425
DB 1402 CTTACTCTCAGTAATGTTTCTATGATGGAAGATCATGCTCAGCTTACAGTGAATCGA 1461
QY 1426 TTCACAAAACCTGGGGTGTGTTTCTCTTGGGAATGGAGAGTCTCAGTGTCTATAAA 1485
DB 1462 TTCACAAAACCTGGGGTGTGTTTCTCTTGGGAATGGAGAGTCTCAGTGTCTATAAA 1521
QY 1486 AATGGTCAGGAATTTCTGTAGCAATGCCCTATATACACTGAAGCATATTTGGATTGAAT 1545
DB 1522 AATGGTCAGGAGATTTCTGTAGCAATGCCCTATATACACTGAAGCATATTTGGATTGAAT 1581
QY 1546 CTTTCTCCATCTGAAAAGTGGTGGAGATTCCTTTATTTGTTGGTAGAGCCCTACAAAT 1605
DB 1582 CTTTCTCCATCTGAAAAGTGGTGGAGATTCCTTTATTTGTTGGTAGAGCCCTACAAAT 1641
QY 1606 AACAGCAATACTATACAGCATACTGCACTACCTTTTTCATTAAGTATGTAATAACTC 1665
DB 1642 AACAGCAATACTATACAGCATACTGCACTACCTTTTTCATTAAGTATGTAATAACTC 1701
QY 1666 TCACCTATTGATGACTATGGGAATTCCTTATGAATCCAGAGATCTAACCCATGCTCTG 1725
DB 1702 TCACCTATTGATGACTATGGGAATTCCTTATGAATCCAGAGATCTAACCCATGCTCTG 1761
QY 1726 TCATCAGAGCCTATGCTATCTATTTCTGAGGCTAGTGATACCAAGCTAAGATCTGATGAT 1785
DB 1762 TCATCAGAGCCTATGCTATCTATTTCTGAGCTAGCGATACAGCTACATACAGAAAT 1821
QY 1786 ATGGATTTTTCGGGACTAAATGTCCTCATATPATGGATGGCAAGGACTTTGGAGTTGGGGC 1845
DB 1822 ATAGATTTTTCGGGACTAAATGTCCTCATPATGGATGGCAAGGACTTTGGAGTTGGGGC 1881
QY 1846 TGGGCAAAACTCAAGATCCAGAACCAAGCATCTTCAGCAACAATCACAGATCCACAAAA 1905
DB 1882 TGGGCAAAACTCAAGATCCAGAACCAAGCATCTTCAGCAACAATCACAGATCCACAAAA 1941
QY 1906 GCCAATAGATCCATAGAACCTTATTTACTGACTTGGCTTCTGCTGGGTATGTTCCCTAGC 1965
DB 1942 GCCAATAGATCCATAGAACCTTACTACTAATAGGCTTCTGCGGGGTATGTTCCCTAGC 2001
QY 1966 CCGAAACACAGAGTCCCTCATAGCAATACCTTATGGGGGAATATGCTGCTTGCAACA 2025

DB 2002 CCAAAACACAGAGTCCCTCATAGCTAAACACCTTATGGGGAATATGCTGCTTGCAACA 2061
QY 2026 GAAAGCTTAAAAAATAGTGAGAACTGACACTAGTGTATCTCTTCTGGGGAAATTACA 2085
DB 2062 GAAAGCTTAAAAAATAGTGAGAACTGACACTAGTGTATCTCTTCTGGGGAAATTACA 2121
QY 2086 GGAGGAGACTAGCATGATGTTTACCAAGATCCTCGAGAAAATCATCTCGGATTCAT 2145
DB 2122 GGAGGAGACTAGCATGATGTTTACCAAGATCCTCGAGAAAATCATCTCGGATTCAT 2181
QY 2146 ATGGCTCTTCCGGATACTCTGCGGGGATGATAGAGGGCAGACACACCTTCTCATTTG 2205
DB 2182 ATGGCTCTTCCGGATACTCTGCGGGGATGATAGAGGGCAGACACACCTTCTCATTTG 2241
QY 2206 AAATTCAGTCAGACCTACACCAAACTCAATGAGCGTTACGCAAAAACCAAGCTATCTCT 2265
DB 2242 AAATTCAGTCAGACCTACACCAAACTCAATGAGCGTTACGCAAAAACCAAGCTATCTCT 2301
QY 2266 AAAAATTAATCTATGCCAAGGAGAAATGCTCTTCTCATTTGCAAGAGGTTTCTTCTGCTGACT 2325
DB 2302 AAAAATTAATCTATGCCAAGGAGAAATGCTCTTCTCATTTGCAAGAGGTTTCTTCTGCTGACT 2361
QY 2326 AAATTAGTTGGCTTTACAGCTATGGAGACCATTAACCTGCTCAACATTTCTATACCAAGGA 2385
DB 2362 AAATTAGTTGGCTTTACAGCTATGGAGACCATTAACCTGCTCAACATTTCTATACTCAAGGA 2421
QY 2386 GAAATCTACATCTCAAGGAGCGTCCGTAGTCAAAAGATGGAGGTCGTGTTTTTTTT 2445
DB 2422 GAAATCTACATCTCAAGGAGCGTCCGTAGTCAAAAGATGGAGGTCGTGTTTTTTTT 2481
QY 2446 GATCTCCTATGAACCTTTGGATCAACGATATACTGACAGCTCCCTTTTATAGTGCT 2505
DB 2482 GATCTCCTATGAACCTTTGGATCAACGATATACTGACAGCTCCCTTTTATAGTGCT 2541
QY 2506 CTTGGTATTTATTTAGCTGCTCTCAGCTTTACTGAGTGGAGGCTATCCCGCAAGCTTT 2565
DB 2542 CTTGGTATTTATTTAGCTGCTCTCAGCTTTACTGAGTGGAGGCTATCCCGCAAGCTTT 2601
QY 2566 TCTCAAGAGACTCCTTTGATCAATGCTCTAGTCCCTATTGGAGTTAAAGGTAGCTTTATG 2625
DB 2602 TCTCAAGAGACTCCTTTGATCAATGCTCTAGTCCCTATTGGAGTTAAAGGTAGCTTTATG 2661
QY 2626 AATGCTACCCAAAGACCTCAAGCCTGGACTGTAGAATGGCATACCAACCCGTTCTGTAT 2685
DB 2662 AATGCTACCCAAAGACCTCAAGCCTGGACTGTAGAATGGCATACCAACCCGTTCTGTAT 2721
QY 2686 AGACAAGAACCAAGGATGCGGACCCAGCTCCTAGCCAGTAAAGGTTATTTGGTTGGTAGT 2745
DB 2722 AGACAAGAACCAAGGATGCGGACCCAGCTCCTAGCCAGTAAAGGTTATTTGGTTGGTAGT 2781
QY 2746 GGAAGCCCTCATCGCTCATGCCATGCTTATATAAATCTCACAGCAACAACCTTTG 2805
DB 2782 GGAAGCCCTCATCGCTCATGCCATGCTTATATAAATCTCACAGCAACAACCTTTG 2841
QY 2806 AGTTGGTTAACTCTCCATTTCCAGTATCATGGATTCTACTCTCTCAACCTTCTGTAAT 2865
DB 2842 AGTTGGTTAACTCTCCATTTCCAGTATCATGGATTCTACTCTCTCAACCTTCTGTAAT 2901
QY 2866 TATCTCAATGGGAAATTTGCTCTCGGATCTAG 2898
DB 2902 TATCTCAATGGGAAATTTGCTCTCGGATCTAG 2934

RESULT 8

ABL92491

ID ABL92491 standard; DNA; 2934 BP.

XX

AC ABL92491;

XX

DT 05-JUN-2002 (first entry)

XX

DE Chlamydia DNA sequence SEQ ID NO:183.

XX Chlamydial infection; Chlamydia; vaccine; detection; diagnosis;
 KW antigen; antibacterial; immunostimulant; immune response;
 KW Chlamydia-specific T-cell response; gene; ds.
 XX Chlamydia sp.
 OS
 XX WO200208267-A2.
 PN
 XX 31-JAN-2002.
 PD
 XX 20-JUL-2001; 2001WO-US23121.
 PF
 XX 20-JUL-2000; 2000US-0620412.
 PR
 XX 23-APR-2001; 2001US-0841132.
 XX (CORI-) CORIXA CORP.
 PA
 XX
 XX Fling SP, Skeiky YAW, Probst P, Bhatia A;
 PI WPI; 2002-179901/23.
 XX
 DR Novel compositions comprising Chlamydia CapI protein and its use in the
 XX treatment of Chlamydia infection -
 PT
 XX Example 1; Page 238-239; 537pp; English.
 PS
 XX The present invention describes compositions comprising a Chlamydia CapI
 CC protein and methods for the diagnosis and therapy of Chlamydia infection.
 CC Chlamydia DNA and protein sequences from the present invention can have
 CC antibacterial and immunostimulant activities, and can be used in
 CC vaccines. Compounds from the present invention can be used for eliciting
 CC an immune response, specifically stimulating a Chlamydia-specific T-cell
 CC response or inhibiting the development of a Chlamydia infection in an
 CC animal. Methods from the present invention can be used: for detecting the
 CC presence of Chlamydia in a patient; to stimulate and/or expand T cells
 CC specific for a Chlamydia protein; and for treatment of a Chlamydia
 CC infection. ABL92394; to ABL92709 and ABB94096 to ABB94374 represent
 CC sequences used in the exemplification of the present invention.
 XX
 SQ Sequence 2934 BP: 875 A; 645 C; 575 G; 839 T; 0 other;

Query Match 95.9%; Score 2777.8; DB 24; Length 2934;
 Best Local Similarity 98.6%; Pred. No. 0;
 Matches 2813; Conservative 0; Mismatches 37; Indels 3; Gaps 1;
 1;
 QY 46 GGACTAGCTAGAGAGGTTCTTCTAGAACTTTCTTATGCGCCCACTCAGTTCCAGATCCT 105
 DB
 QY 85 GGACTAGCTAGAGAGGTTCTTCTAGAACTTTCTTATGCGCCCACTCAGTTCCAGATCCT 144
 DB
 QY 106 ACGAAGAGTCGCTATCAATAAAATAGTTTGACAGGAGACACTCACAACTCTCACTAAC 165
 DB
 QY 145 ACGAAGAGTCGCTATCAATAAAATAGTTTGACAGGAGACACTCACAACTCTCACTAAC 204
 DB
 QY 166 TCGTATCTCGATAACCTAGCTACATACCTTCTTATGCGCCCACTCAGTTCCAGATCCT 225
 DB
 QY 205 TCGTATCTCGATAACCTAGCTACATACCTTCTTATGCGCCCACTCAGTTCCAGATCCT 264
 DB
 QY 226 GCTGCTGTGCACAAATACAGATACCTTCTTATGCGCCCACTCAGTTCCAGATCCT 285
 DB
 QY 265 GCTGCTGTGCACAAATACAGATACCTTCTTATGCGCCCACTCAGTTCCAGATCCT 324
 DB
 QY 286 TTTGCAAAAATCTCACCCCTGAAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 345
 DB
 QY 325 TTTGCAAAAATCTCACCCCTGAAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 384
 DB
 QY 346 CCTACCGTGGAGATTCGTGATACAAATAGCTCCTGTAATCTTTGAAATAAATACTTGTTC 405
 DB
 QY 385 CCTACCGTGGAGATTCGTGATACAAATAGCTCCTGTAATCTTTGAAATAAATACTTGTTC 444
 DB
 QY 406 AGACCATTTACATCGAGTAATCTTAATCGACCTGTTAATAAAATAAGAGGCGGAGCC 465
 DB
 QY 445 AGACTATTTACATGGAGAAATCTTATGCTGCTG---ATAAAATAAGAGGCGGAGCC 501

QY 466 ATTCATGCTCAAAATCTTTACATAAATCATATAATCATGATGTCGCGAATTTATGAAGAAC 525
 DB
 QY 502 ATTCATGCTCAAAATCTTTACATAAATCATATAATCATGATGTCGCGAATTTATGAAGAAC 561
 DB
 QY 526 TTTTCTTATGTCGAGGAGGAGCCATTAGTACCGCTAATACCTTTGTTGTGAGCGAGAAT 585
 DB
 QY 562 TTTTCTTATGTCGAGGAGGAGCCATTAGTACCGCTAATACCTTTGTTGTGAGCGAGAAT 621
 DB
 QY 586 CAGTCTTGTCTCTTTATGGACAACATCTGTATTCAAACTAATAACACAGAGAAAGT 645
 DB
 QY 622 CAGTCTTGTCTCTTTATGGACAACATCTGTATTCAAACTAATAACACAGAGAAAGT 681
 DB
 QY 646 GCGCTATCTATGTCGGAACGAGCAATCTTTTGGAGGTAAATACTGCCATCTCTCTTT 705
 DB
 QY 682 GCGCTATCTATGTCGGAACGAGCAATCTTTTGGAGGTAAATACTGCCATCTCTCTTT 741
 DB
 QY 706 ATCAATAACGCTGTTGTCAGGAGGAGGATCTTCTCCCTATCTGTTCTCTAACAGGA 765
 DB
 QY 742 ATCAATAACGCTGTTGTCAGGAGGAGGATCTTCTCCCTATCTGTTCTCTAACAGGA 801
 DB
 QY 766 AATCGTGTAAACATCGTTTCTATAAACATCGCTCTTTAAATAATGTAAGAACAGCTTCT 825
 DB
 QY 802 AATCGTGTAAACATCGTTTCTATAAACATCGCTCTTTAAATAATGTAAGAACAGCTTCT 861
 DB
 QY 826 TCAGAAGCTTCTGATGGAGGAGCAATTAAGTAACCTACTCGCTAGATGTTTACAGGCAAT 885
 DB
 QY 862 TCAGAAGCTTCTGATGGAGGAGCAATTAAGTAACCTACTCGCTAGATGTTTACAGGCAAT 921
 DB
 QY 886 CGTGGTAGGATCTTTTATGTCACAATATCACAAAAATATGCGGAGCTATTTACGCT 945
 DB
 QY 922 CGTGGTAGGATCTTTTATGTCACAATATCACAAAAATATGCGGAGCTATTTACGCT 981
 DB
 QY 946 CCTAGTATACCTTAGTGGATTAATGGCCCTACTCTTTATAAACAATATCGCCAAATAT 1005
 DB
 QY 982 CCTAGTATACCTTAGTGGATTAATGGCCCTACTCTTTATAAACAATATCGCCAAATAT 1041
 DB
 QY 1006 AAGGGGGCGCTATCTATATAGACGGAACCACTCCAAATTTCTGCGAGCGGCAT 1065
 DB
 QY 1042 AAGGGGGCGCTATCTATATAGACGGAACCACTCCAAATTTCTGCGAGCGGCAT 1101
 DB
 QY 1066 GCTATATTTTAAATGAATAATTTGCACTAATGTAAGTAAATGCAATGTTACAGTACG 1125
 DB
 QY 1102 GCTATATTTTAAATGAATAATTTGCACTAATGTAAGTAAATGCAATGTTACAGTACG 1161
 DB
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 DB
 QY 1162 TCAGCTAATCCTCCTAGAGAAATGCAATAACAGTAGCAGCTCCCTGCTGTAATTTCTA 1221
 DB
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 DB
 QY 1222 TTAGGAGCGGAGTAGCCCAAAATTTAATTTTATGATCCTATTGAAGTTAGCAATGCA 1281
 DB
 QY 1246 GGGTCTCTGTGCTCTCAATAGGAGCTGATCAAAACAGGCTCTGATATTTTTCAGGA 1305
 DB
 QY 1282 GGGTCTCTGTGCTCTCAATAGGAGCTGATCAAAACAGGCTCTGATATTTTTCAGGA 1341
 DB
 QY 1306 GCTACTGTTAAATTCAGATTTTCATCAACGCAATTTTACAACAACAACTGCAACCC 1365
 DB
 QY 1342 GCTACTGTTAAATTCAGATTTTCATCAACGCAATTTTACAACAACAACTGCAACCC 1401
 DB
 QY 1366 CTTACTCTCAGTAATGTTTCTATGATGGAAGATCATGCTCAGCTTACAGTGAATCGA 1425
 DB
 QY 1402 CTTACTCTCAGTAATGTTTCTATGATGGAAGATCATGCTCAGCTTACAGTGAATCGA 1461
 DB
 QY 1426 TTCACACAACCTGGGGGTGTTTCTCTGGAATGAGGAGCTTCTGAGTTGCTATAAA 1485
 DB
 QY 1462 TTCACACAACCTGGGGGTGTTTCTCTGGAATGAGGAGCTTCTGAGTTGCTATAAA 1521
 DB
 QY 1486 AATGGTGCAGGAATTTCTGCTAGCAATGCTTATAAACACTGAAGCATATTTGGATTGAAT 1545
 DB
 QY 1522 AATGGTGCAGGAATTTCTGCTAGCAATGCTTATAAACACTGAAGCATATTTGGATTGAAT 1581

QY 1546 CTTTCTTCATCTCTGAAAGTGGTCTGAGATTCCTTATTGTGGGTAGAGCTACAAAT 1605
DB 1582 CTTTCTTCATCTCTGAAAGTGGTCTGAGATTCCTTATTGTGGGTAGAGCTACAAAT 1641
QY 1606 AACACCAATACTATACAGCAGATCTACTGCGAGTACCTTTTCAATGAAGTGTAAAGCTC 1665
DB 1642 AACACCAATACTATACAGCAGATCTACTGCGAGTACCTTTTCAATGAAGTGTAAAGCTC 1701
QY 1666 TCACATCATGATGACTATGGGAATCTCTTATGAATCCACAGATCTTAACCCATGCTCTG 1725
DB 1702 TCACATCATGATGACTATGGGAATCTCTTATGAATCCACAGATCTTAACCCATGCTCTG 1761
QY 1726 TCATCACAGCCTATGCTATCTATTCTGAGGCTAGTGTAAACAGCTAAGATCTGATGAT 1785
DB 1762 TCATCACAGCCTATGCTATCTATTCTGAGCTAGGATTAACAGCTAAGATCTGATGAT 1821
QY 1786 ATGGATTTTTCGGGACTAAATGTCCCTCATTTATGATGGGCAAGGACTTTGGACTTTGGGC 1845
DB 1822 ATGATTTTTCGGGACTAAATGTCCCTCATTTATGATGGGCAAGGACTTTGGACTTTGGGC 1881
QY 1846 TGGGCAAAACTCAAGATCCAGAACCCAGCATCTTCAGCAACAATCACAGATCCACAAAA 1905
DB 1882 TGGGCAAAACTCAAGATCCAGAACCCAGCATCTTCAGCAACAATCACAGATCCACAAAA 1941
QY 1906 GCCAATAGATTCATAGAACCTTATTACTGACTTGGCTTCCCTGCTGGGTATGTTCCCTAGC 1965
DB 1942 GCCAATAGATTCATAGAACCTTACTACTACATGGCTTCTCGCGGTATGTTCCCTAGC 2001
QY 1966 CGAAACACAGAGTCCCTCATAGCAATACCTTATGGGGGAATATGCTGCTTGCACAA 2025
DB 2002 CCAAAACACAGAGTCCCTCATAGCAATACCTTATGGGGGAATATGCTGCTTGCACAA 2061
QY 2026 GAAAGCTTAAAAATAGTGCAAGACTGACACCTAGTATCATCTTCTGCGGGAATACAA 2085
DB 2062 GAAAGCTTAAAAATAGTGCAAGACTGACACCTAGTATCATCTTCTGCGGGAATACAA 2121
QY 2086 GGAGGAGCTAGGATGATGGTTTACCAGATCTCGAGAAATCATCTCGGATTCAT 2145
DB 2122 GGAGGAGCTAGGATGATGGTTTACCAGATCTCGAGAAATCATCTCGGATTCAT 2181
QY 2146 ATGGCTCTCCGATCTCTGCGGGATGATAGCAGGGCAGACACACCTTCTCATTTG 2205
DB 2182 ATGGCTCTCCGATCTCTGCGGGATGATAGCAGGGCAGACACACCTTCTCATTTG 2241
QY 2206 AAATTCAGTACAGCTACACCAAACTCAATGAGCGTTACGCAAAAAACAAGTATCTCT 2265
DB 2242 AAATTCAGTACAGCTACACCAAACTCAATGAGCGTTACGCAAAAAACAAGTATCTCT 2301
QY 2266 AAAAATCTACTCATGCCAAGGAAATGCTCTTCTCATTTGCAAGAGTTTCTGCTGACT 2325
DB 2302 AAAAATCTACTCATGCCAAGGAAATGCTCTTCTCATTTGCAAGAGTTTCTGCTGACT 2361
QY 2326 AAATTCAGTACAGCTACAGCTATGGAGACCATAACTGTACCAATTTCTATACCAAGGA 2385
DB 2362 AAATTCAGTACAGCTATGGAGACCATAACTGTACCAATTTCTATACCAAGGA 2421
QY 2386 GAAATCTAACTCTCAAGGACCTTCCTGTAGTCAAAACGATGGGAGTGTCTTTTTTTT 2445
DB 2422 GAAATCTAACTCTCAAGGACCTTCCTGTAGTCAAAACGATGGGAGTGTCTTTTTT 2481
QY 2446 GATCCCTATGAACCTTTGGATCAACGATATAGTACAGCTCCCTTTTATAGTGCT 2505
DB 2482 GATCCCTATGAACCTTTGGATCAACGATATAGTACAGCTCCCTTTTATAGTGCT 2541
QY 2506 CTTGGTATTTATCTAGCTGTCTCACTTTACTGAGTGGGAGCTATCCCGAAGCTTT 2565
DB 2542 CTTGGTATTTATCTAGCTGTCTCACTTTACTGAGTGGGAGCTATCCCGAAGCTTT 2601
QY 2566 TCTACAAGACTCTCTTATGATCAATGCTCTAGTCCCTATTGGAGTTAAAGGTAGCTTTATG 2625
DB 2602 TCTACAAGACTCTCTTATGATCAATGCTCTAGTCCCTATTGGAGTTAAAGGTAGCTTTATG 2661
QY 2626 AATGCTACCCAAAGACCTCAAGCCTGGACTGTAGATTGGCATACCAACCGTCTCTGTAT 2685

DB 2662 AATGCTACCCACAGACCTCAAGCCTGGACTGTAGATTGGATACCAACCGTCTGTAT 2721
QY 2686 AGACAAGAACAGGATGCGGACCCAGCTCTAGCCAGTAAGGTAATTTGGTTGGTAGT 2745
DB 2722 AGACAAGAACAGGATGCGGACCCAGCTCTAGCCAGTAAGGTAATTTGGTTGGTAGT 2781
QY 2746 GGAAGCCCTCATCGCTCATGCGCATGCTCTATAAATCTCACAGCAACACACCTTTG 2805
DB 2782 GGAAGCCCTCATCGCTCATGCGCATGCTCTATAAATCTCACAGCAACACACCTTTG 2841
QY 2806 AGTTGGTTAACTCTCCATTTCCAGTATCATGATTCCTCTTCAACCTTCTGTAAT 2865
DB 2842 AGTTGGTTAACTCTCCATTTCCAGTATCATGATTCCTCTTCAACCTTCTGTAAT 2901
QY 2866 TATCTCAATGGGAAATGCTCTCGGATTCAG 2898
DB 2902 TATCTCAATGGGAAATGCTCTCGGATTCAG 2934

RESULT 9

AAD37835
ID AAD37835 standard; DNA; 2871 BP.

XX AAD37835;

XX 27-AUG-2002 (first entry)

XX Chlamydia trachomatis L2 PMPE DNA #2.

XX Polymorphic membrane protein; PMPE; PMPI; vaccine; trachoma; PID; LGV; urethritis; epididymitis; conjunctivitis; cervicitis; cervical cancer; pelvic inflammatory disease; lymphogranuloma venereum; tubal occlusion; endometritis; salpingitis; inflammatory heart disease; cardiomyopathy; infertility; autoimmune myocarditis; atherosclerosis; infection; arthritis; gene; ds.

OS Chlamydia trachomatis.

PH Key Location/Qualifiers
CDS 1..2871
/*tag= a
/product= "Chlamydia trachomatis L2 PMPE protein #2"

XX WO200228998-A2.
XX 11-APR-2002.

XX 28-SEP-2001; 2001WO-US30345.

XX 02-OCT-2000; 2000US-0677752.

XX (ANTE-) ANTEX BIOLOGICS INC.

XX Jackson WJ;

XX WPI: 2002-426107/45.

XX P-PSDB; AAE23486.

XX Novel purified Chlamydia polymorphic membrane protein E or I, useful for preparing vaccines for preventing or treating diseases associated with Chlamydia infection such as trachoma, and infertility -

XX Example; Fig 8; 160pp; English.

XX The invention relates to Chlamydia sp. polymorphic membrane protein (PMP) E and PMPI and nucleic acid molecules encoding such proteins. CC (PMP) and PMPE polypeptides, nucleic acids and vaccines are useful for CC preventing, treating or ameliorating trachoma, conjunctivitis, tubal CC occlusion, cervicitis, cervical cancer, pelvic inflammatory disease CC (PID), lymphogranuloma venereum (LGV), endometritis, epididymitis, CC salpingitis, infertility, reactive arthritis, inflammatory heart CC disease, urethritis, autoimmune myocarditis, cardiomyopathy and

CC atherosclerosis. They are also useful as reagents for clinical or
CC medical diagnosis of Chlamydia infections. The present sequence is
CC Chlamydia trachomatis L2 PMPE DNA.

XX
SQ Sequence 2871 BP; 855 A; 623 C; 567 G; 826 T; 0 other;

Query Match 95.8%; Score 2776.8; DB 24; Length 2871;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 2787; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

QY	94	GTTCAGATCCCTACGNAAGCTCGCTATCAAAATAAAATAGTTTGACAGGAGACACTCAC	153
DB	67	GTTCAGATCCCTACGNAAGAGTCGTATCAAAATAAAATAGTTTGACAGGAGACACTCAC	126
QY	154	AATCTCACAATCGCTATCTCGATACCTACGCTACATACGCTATCTACAAAACCT	213
DB	127	AATCTCACAATCGCTATCTCGATACCTACGCTACATACGCTATCTACAAAACCT	186
QY	214	CCCAATGAAGGAGCTGCTGCTCAATAACAGATTACCTAAGCTTTTGTATACACAAAA	273
DB	187	CCCAATGAAGGAGCTGCTGCTCAATAACAGATTACCTAAGCTTTTGTATACACAAAA	246
QY	274	GAAGGTATTTATTTGCAAAAATCTCACCCCTGAAAGTGGTGGCGATTGGTATGGG	333
DB	247	GAAGGTATTTATTTGCAAAAATCTCACCCCTGAAAGTGGTGGCGATTGGTATGGG	306
QY	334	AGTCCCAATTCCTACCGTGGAGATTCGTGATACAAATAGTCCCTGTAATCTTTGAAAT	393
DB	307	AGTCCCAATTCCTACCGTGGAGATTCGTGATACAAATAGTCCCTGTAATCTTTGAAAT	366
QY	394	AATACTTGTTCGACGACCATTTACATCGAGTAATCCTAATGACGCTGTTAATAAATAAG	453
DB	367	AATACTTGTTCGACGACCATTTACATCGAGTAATCCTAATGACGCTGTTAATAAATAAG	426
QY	454	GAAGGGAGGACCATTCATGCTCAAAATCTTTACATAAATCAATCATGATGTGTCGGA	513
DB	427	GAAGGGAGGACCATTCATGCTCAAAATCTTTACATAAATCAATCATGATGTGTCGGA	486
QY	514	TTTATGAAGAACTTTCTTATGTCGAGGAGGAGCATTTAGTACCGCTAATACCTTTGTT	573
DB	487	TTTATGAAGAACTTTCTTATGTCGAGGAGGAGCATTTAGTACCGCTAATACCTTTGTT	546
QY	574	GTGAGCGAAGTACGCTTGTGTTCTTTATGACAAATCTGTAATCAAACTAATAACA	633
DB	547	GTGAGCGAAGTACGCTTGTGTTCTTTATGACAAATCTGTAATCAAACTAATAACA	606
QY	634	GCAGGAAAGGTGGCGCTATCTATGCTGAACGACCAATTTTTCAGAGTAATACGTC	693
DB	607	GCAGGAAAGGTGGCGCTATCTATGCTGAACGACCAATTTTTCAGAGTAATACGTC	666
QY	694	GATCTCTCTTTATCAATAACGCTGTTGTGAGGAGGAGCATCTTCTCCCTATCTGT	753
DB	667	GATCTCTCTTTATCAATAACGCTGTTGTGAGGAGGAGCATCTTCTCCCTATCTGT	726
QY	754	TCTTAACAGGAAATCGTGGTAACATCGTTTCTATAACAATCGTGTCTTTAAAAATGTA	813
DB	727	TCTTAACAGGAAATCGTGGTAACATCGTTTCTATAACAATCGTGTCTTTAAAAATGTA	786
QY	814	GAACAGCTTCTTCAGAGCTTCTGATGGAGGAGCAATTAAGTAACCTACTCGCTAGT	873
DB	787	GAACAGCTTCTTCAGAGCTTCTGATGGAGGAGCAATTAAGTAACCTACTCGCTAGT	846
QY	874	GTTCAGGCAATCGTGGTAGGATCTTTTATGACAAATATCACAAAAAATTTATGGCGGA	933
DB	847	GTTCAGGCAATCGTGGTAGGATCTTTTATGACAAATATCACAAAAAATTTATGGCGGA	906
QY	934	GCTATTTACGCTCTGTAAGTTACCTAGTGGATAATGGCCCTACCTATTTATAAACAAT	993
DB	907	GCTATTTACGCTCTGTAAGTTACCTAGTGGATAATGGCCCTACCTATTTATAAACAAT	966
QY	994	ATCGGCAATATAAGGGGGCGCTATCTATATAGACGGAACCCAGCACTCCAAAAATCT	1053
DB	967	ATCGGCAATATAAGGGGGCGCTATCTATATAGACGGAACCCAGCACTCCAAAAATCT	1026

QY	1054	GCCGACCGCCATGCTATTTATTTATGAAATATTTGTGACTAATGTAATGCAAT	1113
DB	1027	GCCGACCGCCATGCTATTTATTTATGAAATATTTGTGACTAATGTAATGCAAT	1086
QY	1114	GTACAGTACGTCAGCTAATCTCTAGAGAAATGCAATACAGTACAGCTCCTCT	1173
DB	1087	GTACAGTACGTCAGCTAATCTCTAGAGAAATGCAATACAGTACAGCTCCTCT	1146
QY	1174	GTGAAATCTATAGGAGCAGGAGTACCCAAATTTAATTTTATCATCTATTGAA	1233
DB	1147	GTGAAATCTATAGGAGCAGGAGTACCCAAATTTAATTTTATCATCTATTGAA	1206
QY	1234	GTAGCAATGCAAGGCTCTCTGCTTCAATAGGAAAGCTGATCAAAACAGCTCTGTA	1293
DB	1207	GTAGCAATGCAAGGCTCTCTGCTTCAATAGGAAAGCTGATCAAAACAGCTCTGTA	1266
QY	1294	GTATTTTCAGGAGCTACTGTTAATTCGAGATTTTCATCAACGCAATTTCAACAAAA	1353
DB	1267	GTATTTTCAGGAGCTACTGTTAATTCGAGATTTTCATCAACGCAATTTCAACAAAA	1326
QY	1354	ACACCTGCACCCCTTACTCTCAGTAATGTTTCTTATGTATGAAAGATCATGCTCAGCTT	1413
DB	1327	ACACCTGCACCCCTTACTCTCAGTAATGTTTCTTATGTATGAAAGATCATGCTCAGCTT	1386
QY	1414	ACAGTGAATCGATTCACACAACTGGGGTGTGTTTCTTGGGAATGGAGCAGTTCTG	1473
DB	1387	ACAGTGAATCGATTCACACAACTGGGGTGTGTTTCTTGGGAATGGAGCAGTTCTG	1446
QY	1474	AGTTGCTATAAAAAATGGTGCAGGAAATCTGCTAGCAATGCCTTATAACACTGAAGCAT	1533
DB	1447	AGTTGCTATAAAAAATGGTGCAGGAAATCTGCTAGCAATGCCTTATAACACTGAAGCAT	1506
QY	1534	ATTGATGAATCTTCTTCCATTCGAAAAGTGGTGGCTGAGATTCCTTTATTGGGTA	1593
DB	1507	ATTGATGAATCTTCTTCCATTCGAAAAGTGGTGGCTGAGATTCCTTTATTGGGTA	1566
QY	1594	GAGCTTACAAAATAACAGCAATAACTATACAGCAGATACCTGACGCTACCTTTTCAATAGCT	1653
DB	1567	GAGCTTACAAAATAACAGCAATAACTATACAGCAGATACCTGACGCTACCTTTTCAATAGCT	1626
QY	1654	GATGTAAGTCTACTCATATGATGAGTAATTCCTTATGAATCCACAGATCTA	1713
DB	1627	GATGTAAGTCTACTCATATGATGAGTAATTCCTTATGAATCCACAGATCTA	1686
QY	1714	ACCATGCTCTGCTATCACGCTATGCTATCTATTTCTGAGGCTAGTATACAGCTA	1773
DB	1687	ACCATGCTCTGCTATCACGCTATGCTATCTATTTCTGAGGCTAGTATACAGCTA	1746
QY	1774	AGATCTGATGATGATGATTTTTCGGGACTTAAATGTCCCTCATTTGGATGGCAAGGACTT	1833
DB	1747	AGATCTGATGATGATGATTTTTCGGGACTTAAATGTCCCTCATTTGGATGGCAAGGACTT	1806
QY	1834	TGGATCTGGGGCTGGGCAAAAATCAAGATCCAGAACACAGATCTTTCAGCAACAATCACA	1893
DB	1807	TGGATCTGGGGCTGGGCAAAAATCAAGATCCAGAACACAGATCTTTCAGCAACAATCACA	1866
QY	1894	GATCCACAAAAAGCAATAGATTCCATGAACCTTTTACTGACTTGGCTCTCTGCTGGG	1953
DB	1867	GATCCAAAAAGCAATAGATTCCATGAACCTTTTACTGACTTGGCTCTCTGCTGGG	1926
QY	1954	TATGTTCTAGCCCCGAAACACAGAAAGTCCCTCATAGCGAATACCTTTATGGGGGAATATG	2013
DB	1927	TATGTTCTAGCCCCGAAACACAGAAAGTCCCTCATAGCGAATACCTTTATGGGGGAATATG	1986
QY	2014	CTGCTTTGCAACAGAAAGCTTAAAAAATAGTCAGAACTGACACCTAGTATCATCTCTTC	2073
DB	1987	CTGCTTTGCAACAGAAAGCTTAAAAAATAGTCAGAACTGACACCTAGTATCATCTCTTC	2046
QY	2074	TGGGGAATTTACAGGAGGAGGACTAGGATGATGTTTACCAAGATCCTCGAGAAAAATCAT	2133
DB	2047	TGGGGAATTTACAGGAGGAGGACTAGGATGATGTTTACCAAGATCCTCGAGAAAAATCAT	2106


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QY 241 ACAGATTACCTAAGCTTTTGGATACACAAAAAGAGGTATTATTATTTGCAAAAAATCTC 300
Db 978 ACAGATTACCTAAGCTTTTGGATACACAAAAAGAGGTATTATTATTTGCAAAAAATCTC 919
QY 301 ACCCTGAAAGTGGTGGCGGATTTGGTATGGAGTCCCAATTCCTACCGTGGAGATT 360
Db 918 ACCCTGAAAGTGGTGGCGGATTTGGTATGGAGTCCCAATTCCTACCGTGGAGATT 859
QY 361 CGTGATACAATAGGCTCTGTTTGAATAATACTTTGTGAGGAGCAATTTTACATCG 420
Db 858 CGTGATACAATAGGCTCTGTTTGAATAATACTTTGTGAGGAGCAATTTTACATCG 799
QY 421 AGTAATCTATAGCTGTTTAAATAATAAGAGAGGCGGAGCCATCATCTCAAAAT 480
Db 798 AGAAATCTTATGCTGCTG---ATAAATAAGAGAGGCGGAGCCATCATCTCAAAAT 742
QY 481 CTTTACATAAATCAATCATGATCTGTCGGATTATGAAGAACTTTTATGTCGA 540
Db 741 CTTTACATAAATCAATCATGATCTGTCGGATTATGAAGAACTTTTATGTCGA 682
QY 541 GGAGGAGCCATTAGTACCGCTAATACCTTTGTTGAGCGAGAAATCAGTCTGTTTCTC 600
Db 681 GGAGGAGCCATTAGTACCGCTAATACCTTTGTTGAGCGAGAAATCAGTCTGTTTCTC 622
QY 601 TTTATGGACAACATCTGATTCAAACTAATACAGCAGGAAAAAGTGGCGCTATCTATGCT 660
Db 621 TTTATGGACAACATCTGATTCAAACTAATACAGCAGGAAAAAGTGGCGCTATCTATGCT 562
QY 661 GGAACGAGCAATCTTTGAGAGTAATAACTGCGATCTCTTTTATCAATAACGCCGTGT 720
Db 561 GGAACGAGCAATCTTTGAGAGTAATAACTGCGATCTCTTTTATCAATAACGCCGTGT 502
QY 721 TGTGAGGAGGAGGAGGATCTCTCCCTATCTGTTCTTAACAGGAAAAATCGTGAACATC 780
Db 501 TGTGAGGAGGAGGAGGATCTCTCCCTATCTGTTCTTAACAGGAAAAATCGTGAACATC 442
QY 781 GTTTCTTATAACAATCGCTGCTTTTAAAAATGTAGAAACAGCTTCTTCAAGAGCTTCGAT 840
Db 441 GTTTCTTATAACAATCGCTGCTTTTAAAAATGTAGAAACAGCTTCTTCAAGAGCTTCGAT 382
QY 841 GGAGGAGCAATTAAGTAACCTACTCGCCCTAGATGTTACAGGCAATCGTGGTAGGATCTTT 900
Db 381 GGAGGAGCAATTAAGTAACCTACTCGCCCTAGATGTTACAGGCAATCGTGGTAGGATCTTT 322
QY 901 TTTAGTGACAATATCACAAAAATATATGGCGGAGCTATTTACGCTCCCTGTAGTTACCCCTA 960
Db 321 TTTAGTGACAATATCACAAAAATATATGGCGGAGCTATTTACGCTCCCTGTAGTTACCCCTA 262
QY 961 GTGGATAATGCGCCCTACCTACTTTATAACAATATCGCCAAATAATAAGGGGGCGCTATC 1020
Db 261 GTGGATAATGCGCCCTACCTACTTTATAACAATATCGCCAAATAATAAGGGGGCGCTATC 202
QY 1021 TATATAGACGAAACGAGCAATCCAAATTTCTGCGCGACCGCATGCTATTATTTTAAAT 1080
Db 201 TATATAGACGAAACGAGCAATCCAAATTTCTGCGCGACCGCATGCTATTATTTTAAAT 142
QY 1081 GAAATATTTGACTAATGTAACTAATGCAATGTACCACTAGCTACGCTAAATCTCTCT 1140
Db 141 GAAATATTTGACTAATGTAACTAATGCAATGTACCACTAGCTACGCTAAATCTCTCT 82
QY 1141 AGAAGAAATGCAATAACAGTACGAGCTCTCTGTTGAAATTTCTATTAGGAGCAGGAGT 1200
Db 81 AGAAGAAATGCAATAACAGTACGAGCTCTCTGTTGAAATTTCTATTAGGAGCAGGAGT 22
QY 1201 AGCCAAATTTAATTTTTTAT 1221
Db 21 AGCCAAATTTAATTTTTTAT 1
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RESULT 12
AAD37801
ID AAD37801 standard; DNA; 321 BP.
XX

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AC AAD37801;
XX
DT 27-AUG-2002 (first entry)
XX
XX Chlamydia trachomatis L2 PMPE DNA fragment #2.
XX
XX Polymorphic membrane protein; PMPE; PMPI; vaccine; trachoma; PID; LGV;
XX urethritis; epididymitis; conjunctivitis; cervicitis; cervical cancer;
XX pelvic inflammatory disease; lymphogranuloma venereum; tubal occlusion;
XX endometritis; salpingitis; inflammatory heart disease; cardiomyopathy;
XX infertility; autoimmune myocarditis; atherosclerosis; infection;
XX arthritis; gene; ds.
XX
OS Chlamydia trachomatis.
XX
FH Key Location/Qualifiers
FT CDS 1..321
FT /tag= a
FT /product= "C. trachomatis L2 PMPE protein fragment #2"
FT /note= "CDS does not include start and stop codon"
FT /partial
XX
XX WO200228998-A2.
XX
XX 11-APR-2002.
XX
XX 28-SEP-2001; 2001WO-US30345.
XX
XX 02-OCT-2000; 2000US-0677752.
XX
XX (ANTE-) ANTEX BIOLOGICS INC.
XX
XX Jackson WJ;
XX
XX WPI; 2002-426107/45.
XX
XX P-PSDB; AAE23456.
XX
XX Novel purified Chlamydia polymorphic membrane protein E or I, useful
XX for preparing vaccines for preventing or treating diseases associated
XX with Chlamydia infection such as trachoma, and infertility -
XX
XX Disclosure; Page 143; 160pp; English.
XX
XX The invention relates to Chlamydia sp. polymorphic membrane protein
XX (PMP) E and PMPI and nucleic acid molecules encoding such proteins.
XX PMP and PMPE polypeptides, nucleic acids and vaccines are useful for
XX preventing, treating or ameliorating trachoma, conjunctivitis, tubal
XX occlusion, cervicitis, cervical cancer, pelvic inflammatory disease
XX (PID), lymphogranuloma venereum (LGV), endometritis, epididymitis,
XX salpingitis, infertility, reactive arthritis, inflammatory heart
XX disease, urethritis, autoimmune myocarditis, cardiomyopathy and
XX atherosclerosis. They are also useful as reagents for clinical or
XX medical diagnosis of Chlamydia infections. The present sequence is
XX Chlamydia trachomatis L2 PMPE DNA fragment.
XX
SQ Sequence 321 BP; 101 A; 74 C; 56 G; 90 T; 0 other;
XX
XX Query Match 11.1%; Score 321; DB 24; Length 321;
XX Best Local Similarity 100.0%; Pred. No. 2.8e-80;
XX Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 43 TCAGAGCTAGCTACAGAGGTTCCCTCTAGAAATCTTCTTATGCCCACTCAGTTCCAGAT 102
Db 1 TCAGAGCTAGCTACAGAGGTTCCCTCTAGAAATCTTCTTATGCCCACTCAGTTCCAGAT 60
QY 103 CCTACGAAAGAGTCCGCTATCAATAAATAATTTAGTTTGACAGGAGACACTCAAAATCTCACT 162
Db 61 CCTACGAAAGAGTCCGCTATCAATAAATAATTTAGTTTGACAGGAGACACTCAAAATCTCACT 120
QY 163 AACTGCTATCTCGATAACCTACGCTACATACACTGCTGCTATTCTTACAAAAAATCCCAATGAA 222
Db 121 AACTGCTATCTCGATAACCTACGCTACATACACTGCTGCTATTCTTACAAAAAATCCCAATGAA 180
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QY 223 GGAGCTGCTGTCACATAACAGATTACCTTAAGCTTTTGTATACACAAAAAGAGTATT 282
|||||
Db 181 GGAGCTGCTGTCACATAACAGATTACCTTAAGCTTTTGTATACACAAAAAGAGTATT 240
|||||
QY 283 TATTTTGGCAAAATCTCACCCCTGAAAGTGGTGGCGATTGGTTATCGAGTCCCAAT 342
|||||
Db 241 TATTTTGGCAAAATCTCACCCCTGAAAGTGGTGGCGATTGGTTATCGAGTCCCAAT 300
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QY 343 TCTCCTACCGTGGAGATTGCT 363
|||||
Db 301 TCTCCTACCGTGGAGATTGCT 321
|||||
RESULT 13
AAD37805
ID AAD37805 standard; DNA; 276 BP.
XX
AC AAD37805;
DT 27-AUG-2002 (first entry)
XX
Chlamydia trachomatis L2 PMPE DNA fragment #6.
XX
KW Polymorphic membrane protein; PMPE; PMPI; vaccine; trachoma; PID; LGV;
urethritis; epididymitis; conjunctivitis; cervicitis; cervical cancer;
KW pelvic inflammatory disease; lymphogranuloma venereum; tubal occlusion;
KW endometritis; salpingitis; inflammatory heart disease; cardiomyopathy;
KW infertility; autoimmune myocarditis; atherosclerosis; infection;
KW arthritis; gene; ds.
XX
OS Chlamydia trachomatis.
XX
FH Location/Qualifiers
FT 1..276
FT /*tag= a
FT /product= "c. trachomatis L2 PMPE protein fragment #6"
FT /note= "CDS does not include start and stop codon"
FT /partial
XX
PN WO200228998-A2.
XX
PD 11-APR-2002.
XX
PF 28-SEP-2001; 2001WO-US30345.
XX
PR 02-OCT-2000; 2000US-0677752.
XX
PA (ANTE-) ANTEX BIOLOGICS INC.
XX
PI Jackson WJ;
XX
WPI; 2002-426107/45.
DR P-PSDB; AAE23460.
XX
PT Novel purified Chlamydia polymorphic membrane protein E or I, useful
for preparing vaccines for preventing or treating diseases associated
PT with Chlamydia infection such as trachoma, and infertility -
XX
PS Disclosure; Page 144; 160pp; English.
XX
CC The invention relates to Chlamydia sp. polymorphic membrane protein
CC (PMP) E and PMPI and nucleic acid molecules encoding such proteins.
CC PMPI and PMPE polypeptides, nucleic acids and vaccines are useful for
CC preventing, treating or ameliorating trachoma, conjunctivitis, tubal
CC occlusion, cervicitis, cervical cancer, pelvic inflammatory disease
CC (PID), lymphogranuloma venereum (LGV), endometritis, epididymitis,
CC salpingitis, infertility, reactive arthritis, inflammatory heart
CC disease, urethritis, autoimmune myocarditis, cardiomyopathy and
CC atherosclerosis. They are also useful as reagents for clinical or
CC medical diagnosis of Chlamydia infections. The present sequence is
CC Chlamydia trachomatis L2 PMPE DNA fragment.
XX
SQ Sequence 276 BP; 87 A; 55 C; 53 G; 81 T; 0 other;

Query Match 9.5%; Score 276; DB 24; Length 276;
Best Local Similarity 100.0%; Pred. No. 1.4e-67;
Matches 276; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 823 TCTTCAGAAAGCTTCTGATGGAGAGCAATTAAAGTAAGTAACTACTCGCTAGATGTTACAGGC 882
|||||
Db 1 TCTTCAGAAAGCTTCTGATGGAGAGCAATTAAAGTAAGTAACTACTCGCTAGATGTTACAGGC 60
|||||
QY 883 AATCGTGGTAGGATCTTTTGTAGTACATATACAAAAAATATGCGCGAGCTATTAC 942
|||||
Db 61 AATCGTGGTAGGATCTTTTGTAGTACATATACAAAAAATATGCGCGAGCTATTAC 120
|||||
QY 943 GCTCCTGTAGTTACCTCTAGTGGATATGCGCTACCTACTCTTTATATAACAATATCGCAAT 1002
|||||
Db 121 GCTCCTGTAGTTACCTCTAGTGGATATGCGCTACCTACTCTTTATATAACAATATCGCAAT 180
|||||
QY 1003 AATAAGGGGGCGCTATCTATATAGACGAAACAGCAACTCCAAAATTTCTGCGGACCGC 1062
|||||
Db 181 AATAAGGGGGCGCTATCTATATAGACGAAACAGCAACTCCAAAATTTCTGCGGACCGC 240
|||||
QY 1063 CATGCTATTATTATTAAATGAAATATTGAGCTAAT 1098
|||||
Db 241 CATGCTATTATTATTAAATGAAATATTGAGCTAAT 276
|||||
RESULT 14
AAD37802
ID AAD37802 standard; DNA; 243 BP.
XX
AC AAD37802;
DT 27-AUG-2002 (first entry)
XX
DE Chlamydia trachomatis L2 PMPE DNA fragment #3.
XX
KW Polymorphic membrane protein; PMPE; PMPI; vaccine; trachoma; PID; LGV;
urethritis; epididymitis; conjunctivitis; cervicitis; cervical cancer;
KW pelvic inflammatory disease; lymphogranuloma venereum; tubal occlusion;
KW endometritis; salpingitis; inflammatory heart disease; cardiomyopathy;
KW infertility; autoimmune myocarditis; atherosclerosis; infection;
KW arthritis; gene; ds.
XX
OS Chlamydia trachomatis.
XX
FH Location/Qualifiers
FT 1..243
FT /*tag= a
FT /product= "c. trachomatis L2 PMPE protein fragment #3"
FT /note= "CDS does not include start and stop codon"
FT /partial
XX
PN WO200228998-A2.
XX
PD 11-APR-2002.
XX
PF 28-SEP-2001; 2001WO-US30345.
XX
PR 02-OCT-2000; 2000US-0677752.
XX
PA (ANTE-) ANTEX BIOLOGICS INC.
XX
PI Jackson WJ;
XX
WPI; 2002-426107/45.
DR P-PSDB; AAE23457.
XX
PT Novel purified Chlamydia polymorphic membrane protein E or I, useful
for preparing vaccines for preventing or treating diseases associated
PT with Chlamydia infection such as trachoma, and infertility -
XX
PS Disclosure; Page 143; 160pp; English.
XX

CC The invention relates to Chlamydia sp. polymorphic membrane protein
CC (PMP) E and PMPI and nucleic acid molecules encoding such proteins.
CC PMP and PMPE polypeptides, nucleic acids and vaccines are useful for
CC preventing, treating or ameliorating trachoma, conjunctivitis, tubal
CC occlusion, cervicitis, cervical cancer, pelvic inflammatory disease
CC (PID), lymphogranuloma venereum (LGV), endometritis, epididymitis,
CC salpingitis, infertility, reactive arthritis, inflammatory heart
CC disease, urethritis, autoimmune myocarditis, cardiomyopathy and
CC atherosclerosis. They are also useful as reagents for clinical or
CC medical diagnosis of Chlamydia infections. The present sequence is
CC Chlamydia trachomatis L2 PMPE DNA fragment.

XX SQ Sequence 243 BP; 78 A; 54 C; 44 G; 67 T; 0 other;

Query Match 8.4%; Score 243; DB 24; Length 243;

Best Local Similarity 100.0%; Pred. No. 2.7e-58; Length 243;

Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 133 AGTTTGACGAGACACTCACAATCTCACTAAGTCTATCTCGATAAGCTACGCTACATA 192

Db 1 AGTTTGACGAGACACTCACAATCTCACTAAGTCTATCTCGATAAGCTACGCTACATA 60

Oy 193 CTGGCTATTCTACAAAACCTCCCAATGAAGAGTCTGTGTCACAAATACAGATTACCTA 252

Db 61 CTGGCTATTCTACAAAACCTCCCAATGAAGAGTCTGTGTCACAAATACAGATTACCTA 120

Oy 253 AGCTTTTGTATACAAAAGAGGTATTATTTTGCAGAAATCTCACCCCTGAAGT 312

Db 121 AGCTTTTGTATACAAAAGAGGTATTATTTTGCAGAAATCTCACCCCTGAAGT 180

Oy 313 GGTGTGGATTGGTTATCGGAGTCCCAATCTCTACCCGTGGAGATTCGTGATACATA 372

Db 181 GGTGTGGATTGGTTATCGGAGTCCCAATCTCTACCCGTGGAGATTCGTGATACATA 240

Oy 373 GGT 375

Db 241 GGT 243

RESULT 15

AAD37811

XX AAD37811 standard; DNA; 228 BP.

XX AC AAD37811;

XX DT 27-AUG-2002 (first entry)

XX DE Chlamydia trachomatis L2 PMPE DNA fragment #12.

XX KW Polymorphic membrane protein; PMPE; PMPI; vaccine; trachoma; PID; LGV;
XX urethritis; epididymitis; conjunctivitis; cervicitis; cervical cancer;
XX pelvic inflammatory disease; lymphogranuloma venereum; tubal occlusion;
XX endometritis; salpingitis; inflammatory heart disease; cardiomyopathy;
XX infertility; autoimmune myocarditis; atherosclerosis; infection;
XX arthritis; gene; ds.

XX OS Chlamydia trachomatis.

XX FH Key Location/Qualifiers

XX CDS 1..228

XX FT /*tag= a

XX FT /product= "C. trachomatis L2 PMPE protein fragment #12"

XX FT /note= "CDS does not include start and stop codon"

XX FT /partial

XX PN WO200228998-A2.

XX XX

XX PD 11-APR-2002.

XX XX 28-SEP-2001; 2001WO-US30345.

XX PF 02-OCT-2000; 2000US-067752.

XX XX

PA (ANTE-) ANTEX BIOLOGICS INC.

XX Jackson WJ;

XX WPI; 2002-426107/45.

DR P-PSDB; AAE23466.

XX Novel purified Chlamydia polymorphic membrane protein E or I, useful
XX for preparing vaccines for preventing or treating diseases associated
XX with Chlamydia infection such as trachoma, and infertility -

XX Disclosure; Page 146; 160pp; English.

XX The invention relates to Chlamydia sp. polymorphic membrane protein
CC (PMP) E and PMPI and nucleic acid molecules encoding such proteins.
CC PMP and PMPE polypeptides, nucleic acids and vaccines are useful for
CC preventing, treating or ameliorating trachoma, conjunctivitis, tubal
CC occlusion, cervicitis, cervical cancer, pelvic inflammatory disease
CC (PID), lymphogranuloma venereum (LGV), endometritis, epididymitis,
CC salpingitis, infertility, reactive arthritis, inflammatory heart
CC disease, urethritis, autoimmune myocarditis, cardiomyopathy and
CC atherosclerosis. They are also useful as reagents for clinical or
CC medical diagnosis of Chlamydia infections. The present sequence is
CC Chlamydia trachomatis L2 PMPE DNA fragment.

XX SQ Sequence 228 BP; 73 A; 54 C; 48 G; 53 T; 0 other;

Query Match 7.9%; Score 228; DB 24; Length 228;

Best Local Similarity 100.0%; Pred. No. 4.5e-54;

Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1873 GCATCTTCAGCAACAATCACAGATCCACAAAAGCCCAATAGATTCATAGAACCTTATTA 1932

Db 1 GCATCTTCAGCAACAATCACAGATCCACAAAAGCCCAATAGATTCATAGAACCTTATTA 60

Oy 1933 CTGACTTGGCTTCCTGCTGGGTATGTTCTAGCCGCAACAGAGTCCCTCATAGCG 1992

Db 61 CTGACTTGGCTTCCTGCTGGGTATGTTCTAGCCGCAACAGAGTCCCTCATAGCG 120

Oy 1993 AATACCTTATGGGGGAATATGCTGCTTGCAACAGAAAGCTTAAAAAATAGTGCAGAACTG 2052

Db 121 AATACCTTATGGGGGAATATGCTGCTTGCAACAGAAAGCTTAAAAAATAGTGCAGAACTG 180

Oy 2053 ACACCTAGTGATCATCTCTTCTGGGAATTACAGGAGGAGGACTAGGC 2100

Db 181 ACACCTAGTGATCATCTCTTCTGGGAATTACAGGAGGAGGACTAGGC 228

Search completed: February 4, 2003, 16:35:52

Job time : 2222 secs


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Db 2518 AGCTGCTCACTTTACTAGGTGGAGCCTATCCGGAAGCTTTTCTACAAAGACTCCT 2577
Qy 2581 TTGATCAATAGTCCCTAGTCCCTATTTGGAGTTAAAGGTAGCTTTATGAATGCTTACCCAAAGA 2640
Db 2578 TTGATCAATAGTCCCTAGTCCCTATTTGGAGTTAAAGGTAGCTTTATGAATGCTTACCCACAGA 2637
Qy 2641 CCTCAAGCCTGGAGCTAGAGTGGCATACCAACCCGTTCTGTATAGACAAGAACCAAGG 2700
Db 2638 CCTCAAGCCTGGAGCTAGAGTGGCATACCAACCCGTTCTGTATAGACAAGAACCAAGG 2697
Qy 2701 ATCGGAGCCAGCTCCCTAGCCAGTAAAGGTTATTTGGTTGGTAGTGAAGCCCTCATCG 2760
Db 2698 ATCGGAGCCAGCTCCCTAGCCAGTAAAGGTTATTTGGTTGGTAGTGAAGCCCTCATCG 2757
Qy 2761 CGTCATGCCATGCTTATTAATCTCACAGCAACCAACCTTTGAGTTGGTTAACTCTC 2820
Db 2758 CGTCATGCCATGCTTATTAATCTCACAGCAACCAACCTTTGAGTTGGTTAACTCTC 2817
Qy 2821 CATTTCCAGTATCATGATGATCTACTCTCTTCAACCTTCTGTAATATCTCAATGGGAA 2880
Db 2818 CATTTCCAGTATCATGATGATCTACTCTCTTCAACCTTCTGTAATATCTCAATGGGAA 2877
Qy 2881 ATTGCTCTGGGATTTCTAG 2898
Db 2878 ATTGCTCTGGGATTTCTAG 2895
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RESULT 2

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US-09-620-412C-171
; Sequence 171, Application US/09620412C
; Patent No. 6448234
; GENERAL INFORMATION:
; APPLICANT: Steven P. Fling
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
; FILE REFERENCE: 210121.469C7
; CURRENT APPLICATION NUMBER: US/09/620.412C
; CURRENT FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 363
; SOFTWARE: FastSeq for Windows Version 3.0/4.0
; SEQ ID NO 171
; LENGTH: 2895
; TYPE: DNA
; ORGANISM: Chlamydia
US-09-620-412C-171
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Query Match 97.3%; Score 2821.2; DB 4; Length 2895;
Best Local Similarity 98.6%; Pred. No. 0;
Matches 2857; Conservative 0; Mismatches 38; Indels 3; Gaps 1;

Qy 1 ATGAAAAAGCGTTTCTTTTCTTATTTGGAACTCCCTATCAGGACTAGTAGAG 60
Db 1 ATGAAAAAGCGTTTCTTTTCTTATCGGAACTCCCTATCAGGACTAGTAGAG 60
Qy 61 GTTCCTCTAGAACTTTCTTATGCCAACTCAGTCCAGATCCTACGAAAGAGTCGCTA 120
Db 61 GTTCCTCTAGAACTTTCTTATGCCAACTCAGTCCAGATCCTACGAAAGAGTCGCTA 120
Qy 121 TCAATAAAATAGTTTTCAGAGGAGACACTCACAACTCTCACTAATCTCTCGATAAC 180
Db 121 TCAATAAAATAGTTTTCAGAGGAGACACTCACAACTCTCACTAATCTCTCGATAAC 180
Qy 181 CTAGCTACATACGCTTATCTACAAAAAATCCCAATGAAGAGTCTGTGCACATA 240
Db 181 CTAGCTACATACGCTTATCTACAAAAAATCCCAATGAAGAGTCTGTGCACATA 240
Qy 241 ACAGATTACCTTAAGCTTTTGTATACAAAAAAGAGTATTTATTTGCAAAAAATCTC 300
Db 241 ACAGATTACCTTAAGCTTTTGTATACAAAAAAGAGTATTTATTTGCAAAAAATCTC 300
Qy 301 ACCCCTGAAAGTGTGGGATTTGTTATGCGAGTCCCAATTTCTCTACCGTGAGATT 360
Db 301 ACCCCTGAAAGTGTGGGATTTGTTATGCGAGTCCCAATTTCTCTACCGTGAGATT 360
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Db 301 ACCCCTGAAAGTGTGGGATTTGTTATGCGAGTCCCAATTTCTCTACCGTGAGATT 360
Qy 361 CGTGATACAAATAGTCTCTGTAATCTTTGAAATAAATACCTTTGTTGCGACACCAATTTACATCG 420
Db 361 CGTGATACAAATAGTCTCTGTAATCTTTGAAATAAATACCTTTGTTGCGACACCAATTTACATCG 420
Qy 421 AGTAATCCTAATGAGCTGTGTAATAAATAAGAGAGCGGAGCAATTCATGCTCAAAAT 480
Db 421 AGTAATCCTAATGAGCTGTGTAATAAATAAGAGAGCGGAGCAATTCATGCTCAAAAT 477
Qy 481 CTTTACATAAATACATAATCATGATGCTGGATTTATGAGAACTTTCTTATGTCGGA 540
Db 478 CTTTACATAAATACATAATCATGATGCTGGATTTATGAGAACTTTCTTATGTCGGA 537
Qy 541 GGAGAGCCATTTAGTACCGCTAATACCTTTCTGTTGAGCGAGATCAGTCTGTTTCTC 600
Db 538 GGAGAGCCATTTAGTACCGCTAATACCTTTCTGTTGAGCGAGATCAGTCTGTTTCTC 597
Qy 601 TTTATGACAACTCTGTTATTTCAAACCTAATACAGCAGAAAGGTGGCGCTATCTATGCT 660
Db 598 TTTATGACAACTCTGTTATTTCAAACCTAATACAGCAGAAAGGTGGCGCTATCTATGCT 657
Qy 661 GGAACGAGCAATCTTTTGGAGAGTAATACTGCGATCTCTTTCATCAATAAGCGCTGT 720
Db 658 GGAACGAGCAATCTTTTGGAGAGTAATACTGCGATCTCTTTCATCAATAAGCGCTGT 717
Qy 721 TGTGAGGAGGAGGATCTTCTCCCTATCTGTTCTTAACAGGAAATCGTGGTAACATC 780
Db 718 TGTGAGGAGGAGGATCTTCTCCCTATCTGTTCTTAACAGGAAATCGTGGTAACATC 777
Qy 781 GTTTTCTATAAACAATCGCTGCTTTTAAAAATGTAGAAACAGCTTCTTCAGAGCTTCTGAT 840
Db 778 GTTTTCTATAAACAATCGCTGCTTTTAAAAATGTAGAAACAGCTTCTTCAGAGCTTCTGAT 837
Qy 841 GGAGGAGCAATTAAGTAACCTACTCGCTAGATGTTACAGCAATCGTGGTAGATCTTT 900
Db 838 GGAGGAGCAATTAAGTAACCTACTCGCTAGATGTTACAGCAATCGTGGTAGATCTTT 897
Qy 901 TTTAGTGACAATATCACAAAAAATTTATGGCGAGCTATTTACGCTCTGTAGTTACCTTA 960
Db 898 TTTAGTGACAATATCACAAAAAATTTATGGCGAGCTATTTACGCTCTGTAGTTACCTTA 957
Qy 961 GTGGATAATGGCCCTACTACTTTTATAAACAATATGCCAATAATAAGGGGGCGCTATC 1020
Db 958 GTGGATAATGGCCCTACTACTTTTATAAACAATATGCCAATAATAAGGGGGCGCTATC 1017
Qy 1021 TATATAGAGGAACCAAGCACTCCAAAATTTCTGCCAGCCGCAATGCTATTTTAAAT 1080
Db 1018 TATATAGAGGAACCAAGCACTCCAAAATTTCTGCCAGCCGCAATGCTATTTTAAAT 1077
Qy 1081 GAAATAATTTGTAATAATGTAACCTAATGCAATGTAACCTAATGTAACCTAATGTAACCT 1140
Db 1078 GAAATAATTTGTAATAATGTAACCTAATGCAATGTAACCTAATGTAACCTAATGTAACCT 1137
Qy 1141 AGAAGAAATGCAATAACAGTAGCAAGCTCTCTGTTGAAATTTCTATTAGGAGCAGGAGT 1200
Db 1138 AGAAGAAATGCAATAACAGTAGCAAGCTCTCTGTTGAAATTTCTATTAGGAGCAGGAGT 1197
Qy 1201 AGCCAAAATTTAAATTTTATGATCTTATGAACTTATGAACTTATGAACTTATGAACTTAT 1260
Db 1198 AGCCAAAATTTAAATTTTATGATCTTATGAACTTATGAACTTATGAACTTATGAACTTAT 1257
Qy 1261 TTCAATAAGGAGCTGATCAACAGCTCTGTAATTTTTCAGGAGCTACTGTTAAATCT 1320
Db 1258 TTCAATAAGGAGCTGATCAACAGCTCTGTAATTTTTCAGGAGCTACTGTTAAATCT 1317
Qy 1321 GCAGATTTTCAATCAACCAATTTTACAAACAAAAACCTGCAACCCCTTACTCTCAGTAAT 1380
Db 1318 GCAGATTTTCAATCAACCAATTTTACAAACAAAAACCTGCAACCCCTTACTCTCAGTAAT 1377
Qy 1381 GGTTTCTTATGATCGAAGATCATGCTCAGCTTACAGTGAATCGATTCACACAACTGGG 1440
Db 1378 GGTTTCTTATGATCGAAGATCATGCTCAGCTTACAGTGAATCGATTCACACAACTGGG 1437
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Qy	1441	GGTGTGTTTTCTCTTGGGAATGGAGCAGPTCTGAGTTGCTATATAAAAAATGGTGCAGGAAT	1500
Db	1438	GGTGTGTTTTCTCTTGGGAATGGAGCAGPTCTGAGTTGCTATATAAAAAATGGTACAGGAGAT	1497
Qy	1501	TCGCTAGCAANTGCCCTCTATACACTGAAGCATATTGATTTGAATGAATCTTTCTTCCATTCTG	1560
Db	1498	TCGCTAGCAANTGCCCTCTATAACACTGAAGCATATTGATTTGAATGAATCTTTCTTCCATTCTG	1557
Qy	1561	AAAAAGTGGTCTGAGATTCCCTTTATTGTGGGTAGAGCCTACAAATTAACAGCAATAAATCTAT	1620
Db	1558	AAAAAGTGGTCTGAGATTCCCTTTATTGTGGGTAGAGCCTACAAATTAACAGCAATAAATCTAT	1617
Qy	1621	ACAGCAGATACTGACGCTACCTTTTCATTAAAGTGAATGATAAAGCTCTCAGCTATTGATGAC	1680
Db	1618	ACAGCAGATACTGACGCTACCTTTTCATTAAAGTGAATGATAAAGCTCTCAGCTATTGATGAC	1677
Qy	1681	TATGGGAATTCCTTTTATGAATCCACAGATCTAACCCATGCTCTGTCTATCACAGCCTATG	1740
Db	1678	TACGGGAATTCCTTTTATGAATCCACAGATCTAACCCATGCTCTGTCTATCACAGCCTATG	1737
Qy	1741	CTATCTATTTCTGAGGCTAGTGATACACAGCTTAAGATCTGATGATATGGATTTTTTCGGGA	1800
Db	1738	CTATCTATTTCTGAGGCTAGGCTAAGCATTAACAGCTTAAGATCTGATGATATGGATTTTTTCGGGA	1797
Qy	1801	CTAAATGTCCTCATTTATGGATGGCAAGACTTTGGACTTTGGGCTGGGCAAAAACCTCAA	1860
Db	1798	CTAAATGTCCTCATTTATGGATGGCAAGACTTTGGACTTTGGGCTGGGCAAAAACCTCAA	1857
Qy	1861	GATCCAGAACCCAGCATCTTCACACAAATCAGATCCACAAAAGCCATAGATTCCAT	1920
Db	1858	GATCCAGAACCCAGCATCTTCACACAAATCAGATCCACAAAAGCCATAGATTTCAT	1917
Qy	1921	AGAACCTTATTACTGACTTGGCTTCCGCTGGGTATGTTCTAGCCGGAACACAGAAAT	1980
Db	1918	AGAACCTTACTACTAATGGCTTCCGCGGGTATGTTCTAGCCCAAAACACAGAAAT	1977
Qy	1981	CCCTCATAGCGAATACCTTTATGGGGGAATATGCTGCTTGCAACAGAAAGCTTAAAAAT	2040
Db	1978	CCCTCATAGCTTAACACCTTATGGGGGAATATGCTGCTTGCAACAGAAAGCTTAAAAAT	2037
Qy	2041	AGTGCAAGAACTGACACCTAGTCTATCATCTTTCTGGGGAATTCAGAGGAGGACTAGGC	2100
Db	2038	AGTGCAAGAACTGACACCTAGTCTATCATCTTTCTGGGGAATTCAGAGGAGGACTAGGC	2097
Qy	2101	ATGATGGTTTTACCAAGATCCTCGAGAAATCATCCTGGATTCATATGCGCTCTCCGGA	2160
Db	2098	ATGATGGTTTTACCAAGATCCTCGAGAAATCATCCTGGATTCATATGCGCTCTCCGGA	2157
Qy	2161	TACTCTCGGGGATGATAGCAGGGCAGACACACACCTTCTCATTTGAATTCAGTCAGACC	2220
Db	2158	TACTCTCGGGGATGATAGCAGGGCAGACACACACCTTCTCATTTGAATTCAGTCAGACC	2217
Qy	2221	TACACCAAACTCAATGAGGTTTACGCAAAAACACGATCTCTCTAAAAATTTACTCATGC	2280
Db	2218	TACACCAAACTCAATGAGGTTTACGCAAAAACACGATCTCTCTAAAAATTTACTCATGC	2277
Qy	2281	CAAGGAGAAATGCTCTTCTCATTTGCAAGAAGTTTCTTGCTGACTAAATAGTTGGGCTT	2340
Db	2278	CAAGGAGAAATGCTCTTCTCATTTGCAAGAAGTTTCTTGCTGACTAAATAGTTGGGCTT	2337
Qy	2341	TACAGCTATGGAGACCAATAGTGCACCATTTCTATATCCCAAGGAGAAAATCTAACATCT	2400
Db	2338	TACAGCTATGGAGACCAATAGTGCACCATTTCTATATCCCAAGGAGAAAATCTAACATCT	2397
Qy	2401	CAAGGACCTTCCTGATGCAAAACGATGGAGGTGCTGTTTTTTTTTTGATCTCCCTATGAAA	2460
Db	2398	CAAGGACCTTCCTGATGCAAAACGATGGAGGTGCTGTTTTTTTTTTGATCTCCCTATGAAA	2457
Qy	2461	CCCTTTGGATCAACGCATATACTGACAGCTCCCTTTTTTAGTGCTCTTGATATTTATCT	2520
Db	2458	CCCTTTGGATCAACGCATATACTGACAGCTCCCTTTTTTAGTGCTCTTGATATTTATCT	2517

Qy	2521	AGCCTGTCTCAC	TTTACTGAGTGGGAGGCTAT	CCGCGAAGCTTTTCTTACAAAGACTCCT	2580
Db	2518	AGCCTGTCTCAC	TTTACTGAGTGGGAGGCTAT	CCGCGAAGCTTTTCTTACAAAGACTCCT	2577
Qy	2581	TTGATCAATCTCCT	TAGTCCTATTGGAGTTAAAGT	TAAAGTCTTATGAATGCTTACCCAAGA	2640
Db	2578	TTGATCAATCTCCT	TAGTCCTATTGGAGTTAAAGT	TAAAGTCTTATGAATGCTTACCCAAGA	2637
Qy	2641	CCTCAAGCCCTGG	ACTGTAGAAATTTGGCATACCAAC	CCGTTCTGTATAGACAAGAACCACGAGG	2700
Db	2638	CCTCAAGCCCTGG	ACTGTAGAAATTTGGCATACCAAC	CCGTTCTGTATAGACAAGAACCACGAGG	2697
Qy	2701	ATCGCGACCCAG	CTCTAGCAGTAGAGGATATTTGGT	TTGGTGTAGTGGGAAGCCCTCATCG	2760
Db	2698	ATCGCGACCCAG	CTCTAGCAGTAGAGGATATTTGGT	TTGGTGTAGTGGGAAGCCCTCATCG	2757
Qy	2761	CGTCATGCCATG	TCCCTATAAATCTCACAGCAAA	CACAACTTTGAGTTTGGTTAACTCTC	2820
Db	2758	CGTCATGCCATG	TCCCTATAAATCTCACAGCAAA	CACAACTTTGAGTTTGGTTAACTCTC	2817
Qy	2821	CAATTCCAGTAT	CATGGATTCTACTCCTCTTCAAC	CTTCTGTAAATTAATCTCAATGGGGAA	2880
Db	2818	CAATTCCAGTAT	CATGGATTCTACTCCTCTTCAAC	CTTCTGTAAATTAATCTCAATGGGGAA	2877
Qy	2881	ATTGCTCTGCG	ATTCTAG	2898	
Db	2878	ATTGCTCTGCG	ATTCTAG	2895	

RESULT 3

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RESOL. 2
US-09-556-877-183
: Sequence 183, Application US/09556877
: Patent No. 6432916
: GENERAL INFORMATION:
: APPLICANT: Probst, Peter
: APPLICANT: Bhatia, Ajay
: APPLICANT: Skeiky, Yasir
: APPLICANT: Fling, Steve
: APPLICANT: Maisonneuve, Jeff
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
: TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
: FILE REFERENCE: 210121.469C5
: CURRENT APPLICATION NUMBER: US/09/556,877
: CURRENT FILING DATE: 2000-04-19
: NUMBER OF SEQ ID NOS: 305
: SOFTWARE: FastSeq for Windows Version 3.0/4.0
: SEQ ID NO 183
: LENGTH: 2934
: TYPE: DNA
: ORGANISM: Chlamydia
US-09-556-877-183

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Query Match	95.9%	Score 2777.8;	DB 4;	Length 2934;
Best Local Similarity	98.6%;	Pred. No. 0;		
Matches 2813;	Conservative	0;	Mismatches 37;	Indels 3;
				Gaps 1;

Qy	46	GGACTAGCTAGAGAGGTTCTTCTAGAACTTTCTTATGCCCAACTCAGTTCAGATCCT	105
Db	85	GGACTAGCTAGAGAGGTTCTTCTAGAACTTTCTTATGCCCAACTCAGTTCAGATCCT	144
Qy	106	ACGAAAGAGTCGCTNTCAAAATAAAATAGTTTCACAGGAGACACTCACAACTCTCACTAAC	165
Db	145	ACGAAAGAGTCGCTATCAAAATAAAATAGTTTCACAGGAGACACTCACAACTCTCACTAAC	204
Qy	166	TGCTATCTCGATAACCTACGCTACATCTGGCTATTCTACAAAAACTCCCAATGAAGGA	225
Db	205	TGCTATCTCGATAACCTACGCTACATCTGGCTATTCTACAAAAACTCCCAATGAAGGA	264
Qy	226	GCTGCTCTCAATAACAGATTACCTAAAGCTTTTTTGATACACAAAAAGAGGTATTTAT	285
Db	265	GCTGCTCTCAATAACAGATTACCTAAAGCTTTTTTGATACACAAAAAGAGGTATTTAT	324
Qy	286	TTTGCAAAAAATCTCACCCCTCGAAAGTGGTGGTGGCATTTGGTTATCGGAGTCCCAATCT	345


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QY 2506 CTTGGTATTTATTTCTAGCCCTGTCTCACTTTACTGAGTGGAGCCCTATCCGGAAGCTTT 2565
Db 2542 CTTGGTATTTATTTCTAGCCCTGTCTCACTTTACTGAGTGGAGCCCTATCCGGAAGCTTT 2601
QY 2566 TCTACAAAGACTCCTTTGATCAATGCTCTAGTCCCTATTGGAGTTAAAGTAGCTTTATG 2625
Db 2602 TCTACAAAGACTCCTTTGATCAATGCTCTAGTCCCTATTGGAGTTAAAGTAGCTTTATG 2661
QY 2626 AATGCTACCCAAAGACTCAAGCCTCGACTGTAGATTGATACCAACCCGTTCTGTAT 2685
Db 2662 AATGCTACCCACAGACTCAAGCCTCGACTGTAGATTGATACCAACCCGTTCTGTAT 2721
QY 2686 AGACAAAGAACCGGATCGCGACCCAGCTCTAGCCAGTAAGGGTATTTGGTTTGGTAGT 2745
Db 2722 AGACAAAGAACCGGATCGCGACCCAGCTCTAGCCAGTAAGGGTATTTGGTTTGGTAGT 2781
QY 2746 GGAAGCCCTCATCGCGTATGCCATGCTCTATATAATCTCAGACAAACACACCTTTG 2805
Db 2782 GGAAGCCCTCATCGCGTATGCCATGCTCTATATAATCTCAGACAAACACACCTTTG 2841
QY 2806 AGTTGGTTAACTCCATTCCAGTATCATGGAATCTACTCCTTCAACCTTCTGTAAT 2865
Db 2842 AGTTGGTTAACTCCATTCCAGTATCATGGAATCTACTCCTTCAACCTTCTGTAAT 2901
QY 2866 TATCTCAATGGGGAATTCCTTCGCGATTTCTAG 2898
Db 2902 TATCTCAATGGGGAATTCCTTCGCGATTTCTAG 2934
```

RESULT 4

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US-09-620-412C-183
; Sequence 183, Application US/09620412C
; Patent No. 6448234
; GENERAL INFORMATION:
; APPLICANT: Steven P. Fling
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
; FILE REFERENCE: 210121.469C7
; CURRENT APPLICATION NUMBER: US/09/620,412C
; CURRENT FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 363
; SOFTWARE: FastSeq for Windows Version 3.0/4.0
; SEQ ID NO 183
; LENGTH: 2934
; TYPE: DNA
; ORGANISM: Chlamydia
US-09-620-412C-183
```

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Query Match 95.9%; Score 2777.8; DB 4; Length 2934;
Best Local Similarity 98.6%; Pred. No. 0;
Matches 2813; Conservative 0; Mismatches 37; Indels 3; Gaps 1;

QY 46 GGACTAGCTAGAGAGTTCCTTCTAGAACTTCTTATGCCCACTCAGTCCAGATCCT 105
Db 85 GGACTAGCTAGAGAGTTCCTTCTAGAACTTCTTATGCCCACTCAGTCCAGATCCT 144
QY 106 ACGAAGAGTCTGCTATCAATAAAATTTAGTTTGACAGGAGACACTCACAACTCTCACTAAC 165
Db 145 ACGAAGAGTCTGCTATCAATAAAATTTAGTTTGACAGGAGACACTCACAACTCTCACTAAC 204
QY 166 TCGTATCTCGATAAGCTAGCGTACATACATGCGGTATTCACAAAAAAGTCCCAATGAAGA 225
Db 205 TCGTATCTCGATAAGCTAGCGTACATACATGCGGTATTCACAAAAAAGTCCCAATGAAGA 264
QY 226 GCTGCTGTACAAATACAGATTACCTATTTTGTATACACAAAGAGGTATTAT 285
Db 265 GCTGCTGTACAAATACAGATTACCTATTTTGTATACACAAAGAGGTATTAT 324
QY 286 TTTGCAAAAAATCTCACCCCTGAAAGTGGTGGTGGTATGCGAGTCCCAATCT 345
Db 325 TTTGCAAAAAATCTCACCCCTGAAAGTGGTGGTGGTATGCGAGTCCCAATCT 384
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QY 346 CCTACGCTGGAGATTCGTGATACAATAGGTCTGTATATCTTTGAAAAATAATACTTGTTC 405
Db 385 CCTACGCTGGAGATTCGTGATACAATAGGTCTGTATATCTTTGAAAAATAATACTTGTTC 444
QY 406 AGACCAATTTACATCGAGTAACTCTTAATGAGCTGTTTAATAAATAAGAGCGGAGCC 465
Db 445 AGACTATTTACATGGAGAAATCCTTATGCTGTG--ATAAATAAGAGCGGAGCC 501
QY 466 ATTATGCTCAAAATCTTTACATAAATCAATCATGATGCTGCGGATTTATGAGAAC 525
Db 502 ATTATGCTCAAAATCTTTACATAAATCAATCATGATGCTGCGGATTTATGAGAAC 561
QY 526 TTTTCTTATGCTCCGAGGAGGAGCCATTAGTACCGCTAAATACCTTTTGTGTAGCGAGAAT 585
Db 562 TTTTCTTATGCTCCGAGGAGGAGCCATTAGTACCGCTAAATACCTTTTGTGTAGCGAGAAT 621
QY 586 CAGTCTGTTTCTCTTTATGAGCAACATCTGTATTTCAAACCTAAATACAGCAGGAAAAGT 645
Db 622 CAGTCTGTTTCTCTTTATGAGCAACATCTGTATTTCAAACCTAAATACAGCAGGAAAAGT 681
QY 646 GCGCTATCTATGCTGGAACGAGCAATCTTTTGAGAGTAATAACTGCGATCTCTTCTTT 705
Db 682 GCGCTATCTATGCTGGAACGAGCAATCTTTTGAGAGTAATAACTGCGATCTCTTCTTT 741
QY 706 ATCAATAACGCTGTTGTGAGGAGGAGGATCTTCTCCCTATCTGTGTTCTCTAACAGGA 765
Db 742 ATCAATAACGCTGTTGTGAGGAGGAGGATCTTCTCCCTATCTGTGTTCTCTAACAGGA 801
QY 766 AATCGTGTAACTCGTTTCTTATACAACTCGTCTTTAAAAATGTAGAACAGCTTCT 825
Db 802 AATCGTGTAACTCGTTTCTTATACAACTCGTCTTTAAAAATGTAGAACAGCTTCT 861
QY 826 TCAGAAAGCTTCTGATGGAGGAGCAATTAAGTAAGTACTCGCTAGATCTTTACAGGCAAT 885
Db 862 TCAGAAAGCTTCTGATGGAGGAGCAATTAAGTAAGTACTCGCTAGATCTTTACAGGCAAT 921
QY 886 CCGTGTAGGATCTTTTGTAGTACAAATATCAAAAAAATTTATGGGAGCTATTTACGCT 945
Db 922 CCGTGTAGGATCTTTTGTAGTACAAATATCAAAAAAATTTATGGGAGCTATTTACGCT 981
QY 946 CCGTGTAGTACCTAGTGGATTAATGCCCTACTCTTATAAACAATATCCCAATAT 1005
Db 982 CCGTGTAGTACCTAGTGGATTAATGCCCTACTCTTATAAACAATATCCCAATAT 1041
QY 1006 AAGGGGGCGCTATCTATATAGACGGAACCACTCCAAATTTCTGCCGACCGCCAT 1065
Db 1042 AAGGGGGCGCTATCTATATAGACGGAACCACTCCAAATTTCTGCCGACCGCCAT 1101
QY 1066 GCTATATTTTAAATGAAAAATTTGTGACTAATGTAATGTAATGTAATGTAATGTAATGTA 1125
Db 1102 GCTATATTTTAAATGAAAAATTTGTGACTAATGTAATGTAATGTAATGTAATGTAATGTA 1161
QY 1126 TCAGCTAATCTCTCTAGAGAAATCAATTAACAGTAGCAAGCTCTCTGGTGAATTTCTA 1185
Db 1162 TCAGCTAATCTCTCTAGAGAAATCAATTAACAGTAGCAAGCTCTCTGGTGAATTTCTA 1221
QY 1186 TTAGGAGCAGGAGTAGCCAAATTTTATTTTATGATCTCTTATGAAATTTAGCAATGCA 1245
Db 1222 TTAGGAGCAGGAGTAGCCAAATTTTATTTTATGATCTCTTATGAAATTTAGCAATGCA 1281
QY 1246 GGGGTCTCTGTGCTCTCAATAAGGAAGCTGATCAACAGGCTCTGTAGTATTTTCAGGA 1305
Db 1282 GGGGTCTCTGTGCTCTCAATAAGGAAGCTGATCAACAGGCTCTGTAGTATTTTCAGGA 1341
QY 1306 GCTACTGTTAATTCGACAGATTTTCATCAAGCAATTTACAAACAAACACCTCGACCC 1365
Db 1342 GCTACTGTTAATTCGACAGATTTTCATCAAGCAATTTACAAACAAACACCTCGACCC 1401
QY 1366 CTTACTCTCAGTAAATGGTTTCTATGATCGAAGATCATGCTACGTTTACAGTGAATCGA 1425
Db 1402 CTTACTCTCAGTAAATGGTTTCTATGATCGAAGATCATGCTACGTTTACAGTGAATCGA 1461
QY 1426 TTCACAAACTGGGGGTGTTGTTTCTCTGGGAATGGAGCAGTTCTGAGTTGCTATAAA 1485
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Db	1462	TT	CACAAA	CTGGGG	TGTT	TTCTCT	CTGGAA	TGAG	CAGTCT	CTGAGT	TGCTAT	AAAA	1521				
Qy	1486	AA	TGGT	GCAG	AAAT	TCTG	CTAG	CAAT	GCC	CTATA	CAAC	TGA	AGCATAT	TGGAT	TCAAT	1545	
Db	1522	AA	TGGT	CAGG	AGAT	TCTG	CTAG	CAAT	GCC	CTATA	CAAC	TGA	AGCATAT	TGGAT	TCAAT	1581	
Qy	1546	CT	TTCT	TTCC	AT	TTCT	GAAA	AGTGG	TGCT	GAGAT	TC	CTTT	ATTT	TGTGGG	TAGAG	CCCTAC	1605
Db	1582	CT	TTCT	TTCC	AT	TTCT	GAAA	AGTGG	TGCT	GAGAT	TC	CTTT	ATTT	TGTGGG	TAGAG	CCCTAC	1641
Qy	1606	AA	CAGCA	ATA	ACTAT	ATAC	AGCAT	ACT	CG	AGCT	ACCT	TTT	TCAT	TTA	AGT	GATG	1665
Db	1642	AA	CAGCA	ATA	ACTAT	ATAC	AGCAT	ACT	CG	AGCT	ACCT	TTT	TCAT	TTA	AGT	GATG	1701
Qy	1666	TC	ACT	CA	T	TGAT	GACT	AT	GGG	AA	T	CTCT	CT	AT	T	GAAT	1725
Db	1702	TC	ACT	CA	T	TGAT	GACT	AT	GGG	AA	T	CTCT	CT	AT	T	GAAT	1761
Qy	1726	TC	AT	C	AGC	T	AT	G	T	A	T	T	T	T	T	T	1785
Db	1762	TC	AT	C	AGC	T	AT	G	T	A	T	T	T	T	T	T	1821
Qy	1786	AT	G	A	T	T	T	T	T	T	T	T	T	T	T	T	1845
Db	1822	AT	A	G	A	T	T	T	T	T	T	T	T	T	T	T	1881
Qy	1846	TG	GG	CA	AA	AA	CA	CA	AG	CA	CT	CT	TC	AG	CA	CA	1905
Db	1882	TG	GG	CA	AA	AA	CA	CA	AG	CA	CT	CT	TC	AG	CA	CA	1941
Qy	1906	GC	CA	A	T	A	G	A	T	T	T	T	T	T	T	T	1965
Db	1942	GC	CA	A	T	A	G	A	T	T	T	T	T	T	T	T	2001
Qy	1966	CG	AA	AA	CA	AG	A	G	T	CC	CT	CA	T	AG	CG	AA	2025
Db	2002	CC	AA	AA	CA	AG	A	G	T	CC	CT	CA	T	AG	CG	AA	2061
Qy	2026	GA	AG	CT	T	A	A	A	A	T	G	C	A	A	T	G	2085
Db	2062	GA	AG	CT	T	A	A	A	A	T	G	C	A	A	T	G	2121
Qy	2086	GG	AG	AG	AG	CT	AG	CA	T	GT	GT	T	T	T	T	T	2145
Db	2122	GG	AG	AG	AG	CT	AG	CA	T	GT	GT	T	T	T	T	T	2181
Qy	2146	AT	CG	CT	CT	CG	GA	T	AT	CT	CT	CG	GG	AT	GA	T	2205
Db	2182	AT	CG	CT	CT	CG	GA	T	AT	CT	CT	CG	GG	AT	GA	T	2241
Qy	2206	AA	AT	T	C	AG	T	C	AG	CA	CT	CA	AT	GA	GG	TT	2265
Db	2242	AA	AT	T	C	AG	T	C	AG	CA	CT	CA	AT	GA	GG	TT	2301
Qy	2266	AA	AA	A	T	T	ACT	AT	GC	CA	AG	AA	A	T	T	T	2325
Db	2302	AA	AA	A	T	T	ACT	AT	GC	CA	AG	AA	A	T	T	T	2361
Qy	2326	AA	AT	T	AG	T	GG	G	T	T	T	T	T	T	T	T	2385
Db	2362	AA	AT	T	AG	T	GG	G	T	T	T	T	T	T	T	T	2421
Qy	2386	GA	AA	A	T	T	CA	A	T	C	A	AG	GG	A	T	T	2445
Db	2422	GA	AA	A	T	T	CA	A	T	C	A	AG	GG	A	T	T	2481
Qy	2446	GA	T	CT	CC	CT	AT	GA	A	CC	CT	TT	T	G	A	T	2505
Db	2482	GA	T	CT	CC	CT	AT	GA	A	CC	CT	TT	T	G	A	T	2541
Qy	2506	CT	T	G	G	T	A	T	T	A	T	T	T	T	T		

Db	2542	CTTGGTATTTATTCTAGCGTGTCTCACTTTACTGAGGTGGGAGCCTATCCGCGAAGCTTTT	2601
Qy	2566	TCTACAAGAGACTCCTTTTGATCAATGCTCCCTAGTCCCTATTGGAGTTAAAGGTAGCTTTATG	2625
Db	2602	TCTACAAGAGACTCCTTTTGATCAATGCTCCCTAGTCCCTATTGGAGTTAAAGGTAGCTTTATG	2661
Qy	2626	AATCTCTACCCAAAGACCTCAAGCCTTGGACTGTAGAAATTTGGCATACCAACCCGTTCTGTGAT	2685
Db	2662	AATGCTACCCACAGACCTCAAGCCTTGGACTGTAGAAATTTGGCATACCAACCCGTTCTGTGAT	2721
Qy	2686	AGACAAGAACAGGATTCGGGACCCAGCTCCCTAGCCAGTAAAGGTTATTTGGTTGGTGTAGT	2745
Db	2722	AGACAAGAACAGGATTCGGGACCCAGCTCCCTAGCCAGTAAAGGTTATTTGGTTGGTGTAGT	2781
Qy	2746	GGAAGCCCCATCCTCGGTCTATGCCATGTCCTATATAAATCTTCACAGCAACACCACTTTG	2805
Db	2782	GGAAGCCCCATCCTCGGTCTATGCCATGTCCTATATAAATCTTCACAGCAACACCACTTTG	2841
Qy	2806	AGTTGGTTAACTCTCCATTTCCAGTATCATGGATTCTACTCCTCTTCAACCTTCTGTAAAT	2865
Db	2842	AGTTGGTTAACTCTCCATTTCCAGTATCATGGATTCTACTCCTCTTCAACCTTCTGTAAAT	2901
Qy	2866	TATCTCAATGGGAAATTGCTCTGCGATTCTAG	2898
Db	2902	TATCTCAATGGGAAATTGCTCTGCGATTCTAG	2934
RESULT 5			
US-09-556-877-170			
; Sequence 170, Application US/09556877			
; Patent No. 6432916			
; GENERAL INFORMATION:			
; APPLICANT: Probst, Peter			
; APPLICANT: Bhatia, Ajay			
; APPLICANT: Skeiky, Yasir			
; APPLICANT: Fling, Steve			
; APPLICANT: Maisonneuve, Jeff			
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND			
; TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION			
; FILE REFERENCE: 210121.469C5			
; CURRENT APPLICATION NUMBER: US/09/556,877			
; CURRENT FILING DATE: 2000-04-19			
; NUMBER OF SEQ ID NOS: 305			
; SOFTWARE: FastSeq for Windows Version 3.0/4.0			
; SEQ ID NO 170			
; LENGTH: 2949			
; TYPE: DNA			
; ORGANISM: Chlamydia			
US-09-556-877-170			
Query Match			
Best Local Similarity 1.7%; Score 48.4; DB 4; Length 2949;			
Matches 110; Conservative 0; Mismatches 81; Indels 3; Gaps			

Qy	896	TCTTTTTTACTGACAATACAAAAAATTATGGGGAGCTATTTACGCTCCTCTGTAGTA	955
Db	1001	TTTTCTTTTAGTAGCAATGTAGCTGCTGGAAAGGGGAGCTATTTATGCCAAAAGCTCT	1060
Qy	956	CCCTAGTGGATAATGCCTACCCTACTTTTAAACAATATCGCCAATATAAGGGGGCG	1015
Db	1061	CGGTGTCCTACTGTGGCCCTGTACAATTTTGAAGAATATCGCTAATGAT--GGTGAG	1117
Qy	1016	CTATCTATATAGACGGAAACGAGCAACTCCAAAATTTCTGCCAGCCCATGCTATATTT	1075
Db	1118	CGATTATTTAGGAGAACTCGGAGACCTCAGTTTATCTGCTGATTTATGAGATATATTT	1177
Qy	1076	TTAATGAAATATT	1089
Db	1178	TCGATGGGAATCTT	1191

RESULT 6
US-09-620-412C-170

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; Sequence 170, Application US/09620412C
; Patent No. 6448234
; GENERAL INFORMATION:
; APPLICANT: Steven P. Fling
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
; FILE REFERENCE: 210121.469C7
; CURRENT APPLICATION NUMBER: US/09/620,412C
; CURRENT FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 363
; SOFTWARE: FastSeq for Windows Version 3.0/4.0
; SEQ ID NO 170
; LENGTH: 2949
; TYPE: DNA
; ORGANISM: Chlamydia
US-09-620-412C-170

Query Match 1.7%; Score 48.4; DB 4; Length 2949;
Best Local Similarity 56.7%; Pred. No. 0.001;
Matches 110; Conservative 0; Mismatches 81; Indels 3; Gaps 1;

QY 896 TCTTTTGTAGTACATATACAAAAAATATGCGGAGCTATTTACGCTCCTGTAGTTA 955
Db 1001 TTTCTTTTGTAGTACATATGCTGCGGAGGAGGAGCTATTTATGCCAAAAAGCTCT 1060

QY 956 CCTAGTGGATATGCGCCCTACCTACTTTATAACAATATCGCCAATAATAAGGGGGCG 1015
Db 1061 CGGTTCTTAACCTGTCGCCCTGTACATTTTTRAGGAATATCGCTAATGAT---GGTGGAG 1117

QY 1016 CTATCTATATAGACGGAACCACTCCAAATTTCTCGGACCCCATGTATATTTT 1075
Db 1118 CGATTTATTTAGGAGAACTCGGAGAGCTCAGTTTATCTGCTGATTTATGAGATATTTT 1177

QY 1076 TTAATGAAATATT 1089
Db 1178 TCGATGGGAATCTT 1191

RESULT 7
US-09-556-877-182
; Sequence 182, Application US/09556877
; Patent No. 6432916
; GENERAL INFORMATION:
; APPLICANT: Probst, Peter
; APPLICANT: Bhatia, Ajay
; APPLICANT: Skeiky, Yasir
; APPLICANT: Fling, Steve
; APPLICANT: Maisonneuve, Jeff
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
; FILE REFERENCE: 210121.469C5
; CURRENT APPLICATION NUMBER: US/09/556,877
; CURRENT FILING DATE: 2000-04-19
; NUMBER OF SEQ ID NOS: 305
; SOFTWARE: FastSeq for Windows Version 3.0/4.0
; SEQ ID NO 182
; LENGTH: 3021
; TYPE: DNA
; ORGANISM: Chlamydia
US-09-556-877-182

Query Match 1.7%; Score 48.4; DB 4; Length 3021;
Best Local Similarity 56.7%; Pred. No. 0.001;
Matches 110; Conservative 0; Mismatches 81; Indels 3; Gaps 1;

QY 896 TCTTTTGTAGTACATATACAAAAAATATGCGGAGCTATTTACGCTCCTGTAGTTA 955
Db 1073 TTTTCTTTTGTAGTACATATGCTGCGGAGGAGGAGCTATTTATGCCAAAAAGCTCT 1132

QY 956 CCTAGTGGATATGCGCCCTACCTACTTTATAACAATATCGCCAATAATAAGGGGGCG 1015
Db 1133 CGGTTCTTAACCTGTCGCCCTGTACATTTTTRAGGAATATCGCTAATGAT---GGTGGAG 1189

QY 1016 CTATCTATATAGACGGAACCACTCCAAATTTCTCGGACCCCATGTATATTTT 1075
Db 1190 CGATTTATTTAGGAGAACTCGGAGAGCTCAGTTTATCTGCTGATTTATGAGATATTTT 1249

QY 1076 TTAATGAAATATT 1089
Db 1250 TCGATGGGAATCTT 1263

RESULT 9
US-09-620-412C-316
; Sequence 316, Application US/09620412C
; Patent No. 6448234
; GENERAL INFORMATION:
; APPLICANT: Steven P. Fling
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
; FILE REFERENCE: 210121.469C7
; CURRENT APPLICATION NUMBER: US/09/620,412C
; CURRENT FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 363
; SOFTWARE: FastSeq for Windows Version 3.0/4.0
; SEQ ID NO 316
; LENGTH: 1941
; TYPE: DNA
; ORGANISM: Chlamydia trachomatis
US-09-620-412C-316

Query Match 1.6%; Score 45.2; DB 4; Length 1941;
Best Local Similarity 49.2%; Pred. No. 0.0066;
Matches 239; Conservative 0; Mismatches 233; Indels 14; Gaps 4;

QY 622 CAAACTATACACAGGAAAGGTGCGCTATCTATGCTGGAACGAGCAATTTCTTTTGAG 681
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Db 1114 CAAGCTGAAAATATGGCAGGAGGAGCAATCTGTAGTAGAAGAGACTTGTGCTCAATC 1173
QY 682 AGTAATAACCTGCGATC---TCTTCTTTATCAATAACCCCTGTTGTGCGAGGAGCGCATC 738
Db 1174 AGCAATAATTTCTGGTCCCATAGTTTTTAACATATAACAAGCGGGAAGGTGGAGCTATT 1233
QY 739 TTCTCCCTATCTGTCTCTTAACAGGAAATCGTGGTAACATCGTTTTCTATAACAATCGC 798
Db 1234 AGCGTACCGGATGTGTATTGACAATAACAAGAAGATCATCTTTCAACAATAGT 1293
QY 799 TGTCTTAAATAATAGAAACAGCTTCTCAGAACCTTCTCATGAGGAGGAGCAATTAAGTA 858
Db 1294 TCCTGGGATGGAGCAATCTTCTCT-----GCAAGTAACGAGGAGCGCAATTCAAACG 1347
QY 859 ACTACTCGCTAGATTACAGCAATCGGTAGGATCTTTTGTAGTGACAAATATCACA 918
Db 1348 ACACAGGATTTACTTTACGAATAATAAAGGCTCTATCTACTTTCGACAGCAACATGCT 1407
QY 919 AAAAAATATGGCGAGCTATTTACGCTCTCTGTAGTTACCTAGTGGATAATGGCCCTACC 978
Db 1408 ACACGCGGGGAGCCATTACTGTGGTTACATTGACATCGAGATACGACCGCGTC 1467
QY 979 TACTTTAAACAATATCGCCAATAATAAGGGGGGCGCTATCTATATAGACGGAACGAC 1038
Db 1468 TATTTCTTAATAA-CTCTGCTGCCCTGGGAGCGGCTTTTAATTTATCGAAACGACGTC 1526
QY 1039 AACTCCAAATTTCTCGGACCGCCAT-----GCTATATTTTAAATGAATATTTGGAC 1094
Db 1527 AGCGACAATTTATATCCATACAGGACAGCGGATATGTTTTTAATAATAACGTTGTCT 1586
QY 1095 TAATGT 1100
Db 1587 TACTCT 1592
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RESULT 10

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US-09-620-412C-324
; Sequence 324, Application US/09620412C
; Patent No. 6448234
; GENERAL INFORMATION:
; APPLICANT: Steven P. Fling
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
; FILE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
; FILE REFERENCE: 210121.469C7
; CURRENT APPLICATION NUMBER: US/09/620,412C
; CURRENT FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 363
; SOFTWARE: FastSeq for Windows Version 3.0/4.0
; SEQ ID NO 324
; LENGTH: 1896
; TYPE: DNA
; ORGANISM: Chlamydia trachomatis
US-09-620-412C-324
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Query Match 1.4%; Score 41.4; DB 4; Length 1896;
Best Local Similarity 54.2%; Pred. No. 0.076;
Matches 84; Conservative 0; Mismatches 71; Indels 0; Gaps 0;
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QY 869 TAGATGTTACAGCAATCGGTGGTAGGATCTTTTTTGTAGTACATATACAAAAAATATG 928
Db 1370 TAAAGTTGAAGCAATAAAGGTTCTATTTTGTGATTACAACCTTTGCAAAAGGCAGAG 1429
QY 929 GCGGAGCTATTACGCTCTGTAGTTACCTAGTGGATATGCCCCTACCTACTTTATAA 988
Db 1430 GCGGAGCATCTTAAGCAAGAATCTCTCTGTAGCATGATTCGGTTGTCTTTAGTA 1489
QY 989 ACAATATCGCAATAATAAGGGGGCGCTATCTAT 1023
Db 1490 ACATACAGCAGAAAAGGGGGTGGAGCTATTTAT 1524
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RESULT 11

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RESULT 12
US-09-273-613-3/c
; Sequence 3, Application US/09273613
; Patent No. 6203800
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US-08-915-107-3/c
; Sequence 3, Application US/08915107
; Patent No. 585805
; GENERAL INFORMATION:
; APPLICANT: Burnham, Martin K.R.
; APPLICANT: Lonetto, Michael A.
; APPLICANT: Warren, Patrick V.
; TITLE OF INVENTION: NOVEL Gbpa
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dechert Price & Rhoads
; STREET: 4000 Bell Atlantic Tower, 1717 Arch Stre
; CITY: Philadelphia
; STATE: PA
; COUNTRY: US
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/915,107
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Dickinson, Todd Q
; REGISTRATION NUMBER: 28,354
; REFERENCE/DOCKET NUMBER: P50549-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-994-2252
; TELEFAX: 215-994-2222
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1122 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-08-915-107-3
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Query Match 1.4%; Score 40.6; DB 2; Length 1122;
Best Local Similarity 46.3%; Pred. No. 0.1;
Matches 133; Conservative 0; Mismatches 154; Indels 0; Gaps 0;
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QY 1460 ATGGAGCAGTCTCTGAGTTGCTATATAAAATGGTCAGGAAATCTGTAGCAATGCCTCTA 1519
Db 943 ATTGAGGTGCAGTCATACCTTGTTTAAATGTCGAAGCACGTACTTCTTGACACCAGCAG 884
QY 1520 TAACACTGAAGCATATGGATTGAATCTTTCTCCATCTCTGAAAAGTGGTGGAGATTC 1579
Db 883 TAAATAATGTGTGATAATCTCTTAATTAATTAATTAATTAATTAATTAATTAATTAATCTG 824
QY 1580 CTTTATTGTGGGTAGAGCCCTACAAATAACAGCAATACTATACAGCAGATACTGCAGCTA 1639
Db 823 GTCTTCGATACCTAAATCTCTTAAGNACATTTCTTTATCTCATCATCTAATGTAGCAA 764
QY 1640 CCTTTTCAATTAAGTATGTAATACTCTCACTCAATGATGATGGGAATTCCTCCTTATG 1699
Db 763 TTCTCTTCTCAATTTTTTGGCACTAATAACAATCACTTCAGAGTCTTCTTGGCGTGCATATT 704
QY 1700 AATCCACAGATCTTAACCCATGCTCTGTCTATCAGCGCTATGCTATCT 1746
Db 703 CACGAATCGCTTTTATCTTTATCTATCATCATCATCAATTTTCATCT 657
```

GENERAL INFORMATION:
APPLICANT: Burnham, Martin K.R.
APPLICANT: Lonetto, Michael A.
APPLICANT: Warren, Patrick V.
TITLE OF INVENTION: NOVEL Gbpa
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dechert Price & Rhoads
STREET: 4000 Bell Atlantic Tower, 1717 Arch Stre
CITY: Philadelphia
STATE: PA
COUNTRY: US
ZIP: 19103

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION NUMBER: US/09/273.613
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/915,107
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Dickinson, Todd Q
REGISTRATION NUMBER: 28,354
REFERENCE/DOCKET NUMBER: P50549-4
TELEPHONE: 215-994-2252
TELEFAX: 215-994-2252
TELEX:
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1122 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear

US-09-273-613-3

Query Match 1.4%; Score 40.6; DB 4; Length 1122;

Best Local Similarity 46.3%; Pred. No. 0.1;

Matches 133; Conservative 0; Mismatches 154; Indels 0; Gaps 0;

Qy 1460 ATGGAGCAGTCTGAGTTGCTATATAAATGGTCAGGAAATCTCTAGCAATGCTCTA 1519

Db 943 ATTGAGGTGCAGTCATACCTTGTGTTAAATGTCACAGCAGCTACTTCTTGACACAGCAG 884

Qy 1520 TAACACTGAAGCATATTGGATTGAAATCTTCTTCCATTTCTGAAAAGTGGTCTGAGATT 1579

Db 883 TAAATATGTTGATAATCCTAATATTAATTAATGTCACAGCAGCTACTTCTTGACACAGCAG 824

Qy 1580 CTTTATTCGGGTAGAGCTCAATAACAGCAATACTATACAGCAGATCTGAGCTA 1639

Db 823 GTTCTTCGATACCTAAATCTTCTAAGAACATTTCTTTATCTTCATCATCTAATGAGCAA 764

Qy 1640 CCTTTTCATTAAGTATTAACCTCTCACTCATTTGATGATATGGGAATCTCCTTATG 1699

Db 763 TTTCTTCTTCATTTTTCGACTAATAACATCACTTCAGAGTCTTCTTGGCGCTGCATATT 704

Qy 1700 AATCCAGAGATCTAACCCATCTCTGTGTCATCACGCCCTATGCTATCT 1746

Db 703 CACGAATCGCTTTTACTTTATCATTTATCATCATCATCACCAATTTCACT 657

RESULT 13

US-09-310-867-3/c

Sequence 3, Application US/09310867

Patent No. 6320036

GENERAL INFORMATION:

APPLICANT: Burnham, Martin K.R.

APPLICANT: Lonetto, Michael A.

TITLE OF INVENTION: NOVEL Gbpa

Warren, Patrick V.
TITLE OF INVENTION: NOVEL Gbpa
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dechert Price & Rhoads
STREET: 4000 Bell Atlantic Tower, 1717 Arch Stre
CITY: Philadelphia
STATE: PA
COUNTRY: US
ZIP: 19103

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION NUMBER: US/09/310,867
FILING DATE: 13-May-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/915,107
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Dickinson, Todd Q
REGISTRATION NUMBER: 28,354
REFERENCE/DOCKET NUMBER: P50549-4
TELEPHONE: 215-994-2252
TELEFAX: 215-994-2252
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1122 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear

US-09-310-867-3

Query Match 1.4%; Score 40.6; DB 4; Length 1122;

Best Local Similarity 46.3%; Pred. No. 0.1;

Matches 133; Conservative 0; Mismatches 154; Indels 0; Gaps 0;

Qy 1460 ATGGAGCAGTCTGAGTTGCTATATAAATGGTCAGGAAATCTCTAGCAATGCTCTA 1519

Db 943 ATTGAGGTGCAGTCATACCTTGTGTTAAATGTCACAGCAGCTACTTCTTGACACAGCAG 884

Qy 1520 TAACACTGAAGCATATTGGATTGAAATCTTCTTCCATTTCTGAAAAGTGGTCTGAGATT 1579

Db 883 TAAATATGTTGATAATCCTAATATTAATTAATGTCACAGCAGCTACTTCTTGACACAGCAG 824

Qy 1580 CTTTATTCGGGTAGAGCTCAATAACAGCAATACTATACAGCAGATCTGAGCTA 1639

Db 823 GTTCTTCGATACCTAAATCTTCTAAGAACATTTCTTTATCTTCATCATCTAATGAGCAA 764

Qy 1640 CCTTTTCATTAAGTATTAACCTCTCACTCATTTGATGATATGGGAATCTCCTTATG 1699

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Db 703 CACGAATCGCTTTTACTTTATCATTTATCATCATCATCACCAATTTCACT 657

RESULT 14

US-08-915-107-1/c

Sequence 1, Application US/08915107

Patent No. 5885805

GENERAL INFORMATION:

APPLICANT: Burnham, Martin K.R.

APPLICANT: Lonetto, Michael A.

APPLICANT: Warren, Patrick V.

TITLE OF INVENTION: NOVEL Gbpa

Result	No.	Score	Query		Length	DB	ID	Description
			Match					
c	1	2821.2	97.3	2895	10	US-09-841-132-171	Sequence 171, App	
	2	2777.8	95.9	2934	10	US-09-841-132-183	Sequence 183, App	
	3	1190.6	41.1	1634	12	US-10-007-693-43	Sequence 43, Appl	
	4	115.8	4.0	3092	10	US-09-886-468-9	Sequence 9, Appl	
c	5	48.4	1.7	2949	10	US-09-841-132-170	Sequence 170, App	
	6	48.4	1.7	3021	10	US-09-841-132-182	Sequence 182, App	
	7	45.2	1.6	1941	10	US-09-841-132-316	Sequence 316, App	
	8	41.6	1.4	504	10	US-09-847-539A-16	Sequence 16, Appl	
	9	41.6	1.4	654	10	US-09-847-539A-12	Sequence 12, Appl	
	10	41.6	1.4	764	10	US-09-847-539A-27	Sequence 27, Appl	
	11	41.4	1.4	916	12	US-10-007-693-133	Sequence 133, App	
	12	41.4	1.4	1862	12	US-10-007-693-44	Sequence 44, Appl	
	13	41.4	1.4	1896	10	US-09-841-132-324	Sequence 324, App	
	14	41.4	1.4	3048	12	US-10-007-693-80	Sequence 80, Appl	
	15	40.8	1.4	966	10	US-09-815-242-8052	Sequence 8052, Ap	
	16	40.8	1.4	966	10	US-09-815-242-8678	Sequence 8678, Ap	
	17	40.8	1.4	966	10	US-09-815-242-8966	Sequence 8966, Ap	
	18	40.6	1.4	1098	10	US-09-815-242-4538	Sequence 4538, Ap	
	19	40.6	1.4	1098	10	US-09-815-242-8316	Sequence 8316, Ap	

[illegible]

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being predicted and is derived by analysis of the total score distribution.

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Db 301 ACCCTGAAAGTGGTGGCGGATGGTTATGCGAGTCCCAATTCCTACCGTGGAGATT 360
QY CGTGATACAAATAGGCTCTTAATCTTTGAAAATAATACCTTTGTGGAGACCAATTTACATCG 420
Db 361 CGTGATACAAATAGGCTCTTAATCTTTGAAAATAATACCTTTGTGGAGACTATTACATGG 420
QY AGTAATCTTAATGCGAGCTTTAATAAATAAGAGAGGCGGAGCCATTCATGCTCAAAAT 480
Db 421 AGAAATCTTATGCTGCTG- --ATAAATAAGAGAGGCGGAGCCATTCATGCTCAAAAT 477
QY CTTTACATAAAATCAATAATCATGATGGTGGCGGATTTATGAAGAATCTTTCTTATGTCGA 540
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RESULT 2

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US-09-841-132-183
; Sequence 183, Application US/09841132
; Patent No. US20020061848A1
; GENERAL INFORMATION:
; APPLICANT: Bhatia, Ajay
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Probst, Peter
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
; FILE REFERENCE: 210121.469C8
; CURRENT APPLICATION NUMBER: US/09/841,132
; CURRENT FILING DATE: 2001-04-23
; NUMBER OF SEQ ID NOS: 599
; SOFTWARE: FastSeq for Windows Version 3.0/4.0
; SEQ ID NO 183
; LENGTH: 2934
; TYPE: DNA
; ORGANISM: Chlamydia
US-09-841-132-183
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Query Match 95.9%; Score 2777.8; DB 10; Length 2934;
Best Local Similarity 98.6%; Pred. No. 0;
Matches 2813; Conservative 0; Mismatches 37; Indels 3; Gaps 1;
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QY 1306 GCTACTGTTAAATTTCTGAGATTTTTCATCAACGCAATTTTCAAAACAAAAACACTGCACCC 1365
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Db 1342 GCTACTGTTAAATTTCTGAGATTTTTCATCAACGCAATTTTCAAAACAAAAACACTGCACCC 1401
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[illegible]

RESULT 4

US-09-886-468-9

03 03 000 400 5
: Sequence 9, Application US/09886468; sequence 3, APPLICATION US
; Patent No. US20020037293A1

; FACILEC NO: 032002003
; GENERAL INFORMATION:

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1  APPLICANT: Aventis Pasteur Limited
2  TITLE OF INVENTION: Chlamydia antigens and corresponding DNA fragments and uses ti
3  FILE REFERENCE: 77813-5
4  CURRENT APPLICATION NUMBER: US/09/886,468
5  CURRENT FILING DATE: 1999-12-23
6  PRIOR APPLICATION NUMBER: 60/113,280
7  PRIOR FILING DATE: 1998-12-23
8  PRIOR APPLICATION NUMBER: 60/113,281
9  PRIOR FILING DATE: 1998-12-23
10 PRIOR APPLICATION NUMBER: 60/113,282
11 PRIOR FILING DATE: 1998-12-23
12 PRIOR APPLICATION NUMBER: 60/113,283
13 PRIOR FILING DATE: 1998-12-23
14 PRIOR APPLICATION NUMBER: 60/113,284
15 PRIOR FILING DATE: 1998-12-23
16 PRIOR APPLICATION NUMBER: 60/113,285
17 PRIOR FILING DATE: 1998-12-23
18 PRIOR APPLICATION NUMBER: 60/113,385
19 PRIOR FILING DATE: 1998-12-23
20 PRIOR APPLICATION NUMBER: 60/114,050
21 PRIOR FILING DATE: 1998-12-28
22 PRIOR APPLICATION NUMBER: 60/114,056
23 PRIOR FILING DATE: 1998-12-28
24 PRIOR APPLICATION NUMBER: 60/114,057
25 PRIOR FILING DATE: 1998-12-28
26 PRIOR APPLICATION NUMBER: 60/114,058
27 PRIOR FILING DATE: 1998-12-28
28 PRIOR APPLICATION NUMBER: 60/114,059
29 PRIOR FILING DATE: 1998-12-28
30 PRIOR APPLICATION NUMBER: 60/114,061
31 PRIOR FILING DATE: 1998-12-28
32 NUMBER OF SEQ ID NOS: 26
33 SOFTWARE: PatentIn Ver. 2.0
34 SEQ ID NO 9
35 LENGTH: 3092
36 TYPE: DNA
37 ORGANISM: Chlamydia pneumoniae
38 FEATURE:
39 NAME/KEY: CDS
40 LOCATION: (101)..(2989)
41 US-09-886-468-9

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Qy	901	TTTAGTGACAATATACAAAAAATTATGCGGAGCTATTTACGCTCCTGTAGTTACCCCTA	960
Db	321	TTTAGTGACAATATACAAAAAATTATGCGGAGCTATTTACGCTCCTGTAGTTACCCCTA	262
Qy	961	GTGGATAATGGCCCTACCTACTTTATAACAATATCGCCAATATAAGGGGGCGCTATC	1020
Db	261	GTGGATAATGGCCCTACCTACTTTATAACAATATCGCCAATATAAGGGGGCGCTATC	202
Qy	1021	TATATAGCGGAACCGACCACTCCAAAATTTCTGCCGACCGCCATGCTATTATTTTAAAT	1080
Db	201	TATATAGCGGAACCGAGTAAC'TCCAAAATTTCTGCCGACCGCCATGCTATTATTTTAAAT	142
Qy	1081	GAATAATTTGTGACTAATGTACTAATGCAAAATGGTACCAAGTACGTACGTAAATCCTCCT	1140
Db	141	GAATAATTTGTGACTAATGTACTAATGCAAAATGGTACCAAGTACGTACGTAAATCCTCCT	82
Qy	1141	AGAAGAAATGCAATTAACAGTACGAAGCTCCTCTGCTGAAATTCATTATAGGAGCAGGGAGT	1200
Db	81	AGAAGAAATGCAATTAACAGTACGAAGCTCCTCTGCTGAAATTCATTATAGGAGCAGGGAGT	22
Qy	1201	AGCCAAAATTTAATTTTTTAT	1221
Db	21	AGCCAAAATTTAATTTTTTAT	1


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; FILE REFERENCE: 210121.469C8
; CURRENT APPLICATION NUMBER: US/09/841.132
; CURRENT FILING DATE: 2001-04-23
; NUMBER OF SEQ ID NOS: 599
; SOFTWARE: FastSeq for Windows Version 3.0/4.0
; SEQ ID NO 182
; LENGTH: 3021
; TYPE: DNA
; ORGANISM: Chlamydia
US-09-841-132-182

Query Match          1.7%; Score 48.4; DB 10; Length 3021;
Best Local Similarity 56.7%; Pred. No. 0.005;
Matches 110; Conservative 0; Mismatches 81; Indels 3; Gaps 1;

QY 896 TCTTTTGTAGTGAATATCACAAAATATATGCGGAGCTATTAGCCTCTCTAGCTTA 955
Db 1073 TTTTCTTTTAGTGAATATGTTAGTCTGCTGGAAAGGGGAGCTATTATGCCAAAAGCTCT 1132
QY 956 CCCTAGTGGATAATGCGCCCTACCTACTTTATAACAATATCGCCAATATAAAGGGGGCG 1015
Db 1133 CGGTTGCTAACTGTGGCCCTGTACAATTTTAAGGAATATCGCTAATGAT---GGTGGAG 1189
QY 1016 CTATCTATATAGCGGAACAGCAACTCCAAAATTTCTCGGAGCCGCCATGCTATTATTT 1075
Db 1190 CGATTATTTAGGAGAATCTGGAGAGCTCAGTTTATCTGCTGATTATGGAGATATTATTT 1249
QY 1076 TTAATGAAATATT 1089
Db 1250 TCGATGGGAATCTT 1263

RESULT 7
US-09-841-132-316
; Sequence 316, Application US/09841132
; Patent No. US20020061848A1
; GENERAL INFORMATION:
; APPLICANT: Bhatia, Ajay
; APPLICANT: Skeiky, Yajay A.W.
; APPLICANT: Probst, Peter
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
; DIAGNOSIS OF CHLAMYDIAL INFECTION
; FILE REFERENCE: 210121.469C8
; CURRENT APPLICATION NUMBER: US/09/841.132
; CURRENT FILING DATE: 2001-04-23
; NUMBER OF SEQ ID NOS: 599
; SOFTWARE: FastSeq for Windows Version 3.0/4.0
; SEQ ID NO 316
; LENGTH: 1941
; TYPE: DNA
; ORGANISM: Chlamydia trachomatis
US-09-841-132-316

Query Match          1.6%; Score 45.2; DB 10; Length 1941;
Best Local Similarity 49.2%; Pred. No. 0.03;
Matches 239; Conservative 0; Mismatches 233; Indels 14; Gaps 4;

QY 622 CAACACTAATACAGAGAAAGGTGGCGCTATCTATCTGGAAGGAGCAATCTTTTGGAG 681
Db 1114 CAAGCTGAAATATGGCACGAGGAGGAGCAATCTGTAGTAGAAGAGACTTGTGCTCAATC 1173
QY 682 AGTAATAACTCGGATC---TCTTCTTTTATCAATAACGCCCTGTCTGCGAGGAGGCGATC 738
Db 1174 AGCAATATCTGCTGCCATAGTTTTTAACTATAACCAAGCGGGGAAAGGTGGAGCTATT 1233
QY 739 TTTCTCCCTATCTGTTCTCTAACAGGAAATCGTGGTAACATCGTTTTTCTATACAAATCGC 798
Db 1234 AGCGCTACCGGATGTGTTATGACATAACAAGAAAGATCATCTTTTCAACAAATAGT 1293
QY 799 TGCTTTAAAATGTAGAACAGCTTCTTCAGAGCTTCTGATGGAGCAATTAAGTA 858
Db 1294 TCCTGGGATGGAGCCAACTCTTCTCT-----GCAAGTAACGAGGAGGAGCCATTCAAACG 1347
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QY 859 ACTACTCGCCTAGATGTTACAGGCAATCGTGGTAGGATCTTTTTTACTGACAATATCACA 918
Db 1348 ACACAAGGATTTACTTTTACGAATAATAAAGGCTCTATCTACTTCGACAGCAACACTGCT 1407
QY 919 AAAAATTATGGCGAGCTATTAGCTCCTGTAGTTACCTTAGTGGAATATGGCCCTTACC 978
Db 1408 ACACACGCGGGGAGCCATTAACGTGTGTACATTGACATCCGAGATAACGGACCGCTC 1467
QY 979 TACTTTATAACATATATCGCAATAATAAAGGGGGCGCTATCTATATAGACGGAACACGC 1038
Db 1468 TATTTTCTAATAAA-CTCTGCTGCTGGGAGCGGCTTTAATTTATCGAAACACCTTC 1526
QY 1039 AACTCCAAAATTTCTGCGGACCGCCAT---GCTATTATTTTAAATGAAAATATTTGTGAC 1094
Db 1527 AGCGACAAATATATCATACAGGACAGGAGATATTTGTTTTTAATAATAACGTTGTCTT 1586
QY 1095 TAATGT 1100
Db 1587 TACTCT 1592

RESULT 8
US-09-847-539A-16
; Sequence 16, Application US/09847539A
; Patent No. US20020061306A1
; GENERAL INFORMATION:
; APPLICANT: Bjorck, Lars H
; APPLICANT: Rasmussen, Magnus
; TITLE OF INVENTION: STREPTOCOCCAL ALPHA 2M BINDING PROTEIN
; FILE REFERENCE: 100084.415US / N.75312B
; CURRENT APPLICATION NUMBER: US/09/847.539A
; CURRENT FILING DATE: 2001-05-01
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 504
; TYPE: DNA
; ORGANISM: Streptococcus pyogenes
US-09-847-539A-16

Query Match          1.4%; Score 41.6; DB 10; Length 504;
Best Local Similarity 50.0%; Pred. No. 0.14;
Matches 104; Conservative 0; Mismatches 104; Indels 0; Gaps 0;

QY 1119 CAGTACGTCAGCTAATCCTCTAGAGAATAAGCAATACAGTAGCAGCTCCTCTGCTGA 1178
Db 75 CGGAACCTTAACATACTCTTGGCAATGCTCCAGAAAAAAGCTGCAATTACGTAATGAAGA 134
QY 1179 AATTCTATTAGGAGCAGGAGTAGCCAAAATTTAATTTTTTATGATCCTATTGAAAGTAG 1238
Db 135 AAGAGCCATTGATGAATTAATAAACAAGCTATTGAGGATAAAGAAGCTACGACAGCTAT 194
QY 1239 CAATGCGAGGCTCTCTGTGCTTCAATAAGGAAGTGTATCAACAGGCTCTGTAGTATT 1298
Db 195 AGAAGCAGCAAGTTCAGATGCTTTAGAACGATTAGCGGATCAACACAGACGCTTTACAATC 254
QY 1299 TTGAGGAGCTACTGTTTAATTTCTGCAGAT 1326
Db 255 AGAAGAGCTGCGGTTTGTGTTAAAGCGGAT 282

RESULT 9
US-09-847-539A-12
; Sequence 12, Application US/09847539A
; Patent No. US20020061306A1
; GENERAL INFORMATION:
; APPLICANT: Bjorck, Lars H
; APPLICANT: Rasmussen, Magnus
; TITLE OF INVENTION: STREPTOCOCCAL ALPHA 2M BINDING PROTEIN
; FILE REFERENCE: 100084.415US / N.75312B
; CURRENT APPLICATION NUMBER: US/09/847.539A
; CURRENT FILING DATE: 2001-05-01
; NUMBER OF SEQ ID NOS: 30
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; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Probst, Peter
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
; FILE REFERENCE: 210121.469C8
; CURRENT APPLICATION NUMBER: US/09/841.132
; CURRENT FILING DATE: 2001-04-23
; NUMBER OF SEQ ID NOS: 599
; SOFTWARE: FastSEQ for Windows Version 3.0/4.0
; SEQ ID NO 324
; LENGTH: 1896
; TYPE: DNA
; ORGANISM: Chlamydia trachomatis
US-09-841-132-324

Query Match          1.4%; Score 41.4; DB 10; Length 1896;
Best Local Similarity 54.2%; Pred. No. 0.33;
Matches 84; Conservative 0; Mismatches 71; Indels 0; Gaps 0;

Qy 869 TAGATGTTACAGGCAATCGTGTAGGATCTTTTTTAGTACAAATATCAGGCAATATG 928
    || || ||||| || || ||||| ||||| ||||| ||||| ||||| |||||
Db 1370 TAAAGTTGAAGGCAATAAAGGTTCTATTGTTTGTGATTACAACTTTGCAAAAGGCAGAG 1429
    || || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy 929 GCGGAGCTATTACGCTCCTAGTACCCCTAGTGGGATATGCGCCCTACCTACTTTATAA 988
    ||||| || || || || || || || || || || || || || || || || || || ||
Db 1430 GCGGAAGCATCCTAACGAAAGAAATCTCTCTGTAGCAGATGATTCGGTGTCTTTAGTA 1489
    ||||| || || || || || || || || || || || || || || || || || || ||

Qy 989 ACAATATCGGCAATAAAGGGGCGCTATCTAT 1023
    ||||| || || || || || || || || || || || || || || || || || || ||
Db 1490 ACAATACAGCAGAAAAGGCGGTGGAGCTATTAT 1524
    ||||| || || || || || || || || || || || || || || || || || || ||

RESULT 14
US-10-007-693-80
; Sequence 80, Application US/10007693
; Patent No. US20020146776A1
; GENERAL INFORMATION:
; APPLICANT: Bhatia, Ajay
; APPLICANT: Probst, Peter
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR TREATMENT
; TITLE OF INVENTION: AND DIAGNOSIS OF CHLAMYDIAL INFECTION
; FILE REFERENCE: 210121.515C2
; CURRENT APPLICATION NUMBER: US/10/007.693
; CURRENT FILING DATE: 2001-12-05
; NUMBER OF SEQ ID NOS: 157
; SEQ ID NO 80
; LENGTH: 3048
; TYPE: DNA
; ORGANISM: Chlamydia trachomatis serovar D
US-10-007-693-80

Query Match          1.4%; Score 41.4; DB 12; Length 3048;
Best Local Similarity 54.2%; Pred. No. 0.43;
Matches 84; Conservative 0; Mismatches 71; Indels 0; Gaps 0;

Qy 869 TAGATGTTACAGGCAATCGTGTAGGATCTTTTTTAGTACAAATATCAGGCAATATG 928
    || || ||||| || || ||||| ||||| ||||| ||||| ||||| |||||
Db 929 TAAAGTTGAAGGCAATAAAGGTTCTATTGTTTGTGATTACAACTTTGCAAAAGGCAGAG 988
    || || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy 929 GCGGAGCTATTACGCTCCTAGTACCCCTAGTGGGATATGCGCCCTACCTACTTTATAA 988
    ||||| || || || || || || || || || || || || || || || || || || ||
Db 989 GCGGAAGCATCCTAACGAAAGAAATCTCTCTGTAGCAGATGATTCGGTGTCTTTAGTA 1048
    ||||| || || || || || || || || || || || || || || || || || || ||

Qy 989 ACAATATCGGCAATAAAGGGGCGCTATCTAT 1023
    ||||| || || || || || || || || || || || || || || || || || || ||
Db 1049 ACAATACAGCAGAAAAGGCGGTGGAGCTATTAT 1083
    ||||| || || || || || || || || || || || || || || || || || || ||

RESULT 15
US-09-815-242-8052
; Sequence 8052, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; TITLE OF INVENTION: Prokaryotes
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815.242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8052
; LENGTH: 966
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(966)
US-09-815-242-8052
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Query Match          1.4%; Score 40.8; DB 10; Length 966;
Best Local Similarity 44.7%; Pred. No. 0.33;
Matches 159; Conservative 0; Mismatches 197; Indels 0; Gaps 0;

Qy 1223 ATCCATTATGAAGTTAGCAATGCAGGGGTCTCTGTGTCTCTCAATAAGCAAGCTGATCAA 1282
    || || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 302 ATGCAAGACAGATAGAAAAGCCCGTAGCCGTGAGCCAATCACTGCTAAATTAGTTGCAA 361
    || || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy 1283 CAGGCTCTGTAGTATTTTCAGGAGCTACTGTTAATCTGCAGATTTTCATCAACGCAATT 1342
    || || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 362 ACTTAATCGAAACAGCTGGGCAACTCGTATGATTGCGTTAGACTTACATGCACCAAAA 421
    || || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy 1343 TACAAAACAAAACACCTGCACCCCTTACTCTCAGTAATGGTTTCTATGTATCGAAGATC 1402
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 422 TTCAAGGATCTTTGATATTCCAAATGACCACCTTAATGGGTGTCCTTAATCTTGTCTAAAC 481
    || || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy 1403 ATGCTCAGCTTACAGTGAATTCACAAAACCTGCGGGGTGTGTTTCTCTCTGGGAATG 1462
    || || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 482 ATTTCAAAGATGATCCGAATATTAAACCAGAGAAATGTCGTGTTTTCACCAGACCATG 541
    || || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy 1463 GAGCAGTCTGAGTGTGTATATAAAATGGTGAGGAAATTCGTGAGCAATGCCTCTATAA 1522
    || || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 542 GCGGTGTTACACGCTGCACGTAATTTAGCTGACATTTTAAAAAACTCCCAATTCGAATTAG 601
    || || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy 1523 CACTGAAGCATATGGGATTTGAATCTTTCTTCCATTTCTGAAAAGTGGTGCAGATT 1578
    || || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 602 ATAAACCTCGTCCTAGACCAAAATGTTGCTGAAGTGATGAACATTTGTTGGTGAGATT 657
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Search completed: February 4, 2003, 20:53:39
Job time : 189 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: February 4, 2003, 15:57:07 ; Search time 3573 Seconds
(without alignments)
13135.886 Million cell updates/sec

Title: US-09-677-752-1
Perfect score: 2898
Sequence: 1 atgaaaaagcgtttttttt.....aaattgctctgcgacttag 2898

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues
Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpi:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
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25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
c 1	49.6	1.7	1101	17	CNS0039G	AL063921 Drosophila
c 2	44.6	1.5	667	13	BJ390296	BJ390296 BJ390296
c 3	44.6	1.5	806	17	CNS04AEE	AL281759 Tetraodon
c 4	44	1.5	594	10	AW109947	AW109947 MT16306 m
c 5	44	1.5	1011	17	CNS0205Y	AL175183 Tetraodon
c 6	43.8	1.5	531	13	BJ438828	BJ438828 BJ438828

7	43.8	1.5	597	9	AU261972	AU261972 AU261972
c 8	43.2	1.5	730	17	BH597226	BH597226 BOHPJ06TF
c 9	43	1.5	968	17	CNS006R5	AL065820 Drosophila
10	42.8	1.5	600	14	B0595967	B0595967 PfESTOab2
11	41.6	1.4	538	17	AZ068468	AZ068468 RPCI-23-4
12	41.4	1.4	1101	17	CNS0182P	AL108811 Drosophila
13	41.2	1.4	667	12	BF298817	BF298817 021PBG02
c 14	41	1.4	312	13	BJ438184	BJ438184 BJ438184
c 15	41	1.4	615	13	BJ355703	BJ355703 BJ355703
c 16	41	1.4	613	13	BJ425106	BJ425106 BJ425106
c 17	41	1.4	1101	17	CNS017DP	AL107911 Drosophila
18	40.6	1.4	522	13	B1815912	B1815912 PfESTOa3
c 19	40.6	1.4	602	17	DR7024T	BI815588 Danio rer
c 20	40.6	1.4	891	17	AZ529319	AZ529319 ENT8K28TR
c 21	40.6	1.4	919	17	AZ669216	AZ669216 ENTHP96TR
c 22	40.4	1.4	575	17	AQ981798	AQ981798 RPCI-23-3
c 23	40.2	1.4	487	17	AZ900612	AZ900612 RPCI-24-1
c 24	40.2	1.4	562	17	PT013K11R	AL446148 Paramediu
c 25	40	1.4	493	17	AA550487	AA550487 1642m3 gm
c 26	39.8	1.4	324	14	F07305	F07305 HSC21G011 n
27	39.8	1.4	350	9	AU060746	AU060746 AU060746
28	39.8	1.4	388	9	AI831292	AI831292 WJ82802.x
29	39.8	1.4	420	9	AJ280396	AJ280396 4A3A-AAO
c 30	39.8	1.4	483	13	BJ405337	BJ405337 BJ405337
c 31	39.8	1.4	679	14	BM728778	BM728778 UI-E-E01-
c 32	39.6	1.4	409	10	BE580247	BE580247 kq38h11.y
33	39.6	1.4	603	17	AQ439611	AQ439611 HS_5121.A
34	39.6	1.4	1101	17	CNS00GDR	AL072060 Drosophila
35	39.4	1.4	306	9	AA094179	AA094179 cl2060.se
36	39.4	1.4	526	13	B1814808	BI814808 PfESTOa0
37	39.4	1.4	596	17	AQ803690	AQ803690 HS_3175.A
c 38	39.2	1.4	410	12	BE834190	BE834190 RCI-OT008
39	39.2	1.4	451	9	AU268963	AU268963 AU268963
40	39.2	1.4	643	13	BJ422941	BJ422941 BJ422941
41	39.2	1.4	685	12	BF276133	BF276133 GA_EB002
c 42	39.2	1.4	723	13	BJ434535	BJ434535 BJ434535
c 43	39.2	1.4	801	14	C24322	C24322 C24322 Dict
44	39.2	1.4	894	17	AZ529017	AZ529017 ENT0V44TF
c 45	39.2	1.4	1074	17	CNS07E9K	AL441486 T3 end of

ALIGNMENTS

RESULT 1
CNS0039G/c 1101 bp DNA linear GSS 03-JUN-1999
LOCUS Drosophila melanogaster genome survey sequence TET3 end of BAC #
DEFINITION BACR08K10 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.
ACCESSION AL063921 GI:4941778
VERSION AL063921
KEYWORDS Drosophila melanogaster.
SOURCE Drosophila melanogaster.
ORGANISM Drosophila melanogaster.
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE Direct Submission
AUTHORS Submitted (02-JUN-1999) Genoscope - Centre National de Sequençage :
TITLE Bp 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)
JOURNAL - Web : www.genoscope.cns.fr)
COMMENT Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see <http://www.fruitfly.org> The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osogawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial

EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's p1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

FEATURES
Source
1. 1101
/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone="BACR08K10"
/clone_lib="RPCI-98"
/note="end : TET3"

BASE COUNT 201 a 64 c 131 g 202 t 503 others
ORIGIN

Query Match 1.7%; Score 49.6; DB 17; Length 1101;
Best Local Similarity 16.7%; Pred. NO. 0.023;
Matches 88; Conservative 238; Mismatches 198; Indels 4; Gaps 2;

Qy 1064 ATGCTATTATTTTAAATGAAATATGTCACAAATGTAACAAATGTCACAGTA 1123
Db 1088 DTRKDDWMTKWTWKDRADRRWAGDADRWDGAGTWTATWWWWWWATWDTW 1029

Qy 1124 CGTCAGCAATCTCTAGAGAAATGCAATAACAGTAGCAGCTCCTCTGCTGAAATTC 1183
Db 1028 DKWWWATAAKTDTATWRTAWRADWAGRGAGKRDRAATDADGAGRRDGRKDK 969

Qy 1184 TATTAGGACGAGGAGTAGCCAAAATTTAATTTTATGATCCTATTCGAAGTACGAATG 1243
Db 968 KDRKDGDDDKGKKKAAKAAKWTAKWDDWDWDKWKGAKDKADDDDDGAGDKDD 909

Qy 1244 CAGGGGCTCTGCTGCTTCAATAGGAGCTGATCAACAGGCTCTGTAGTATTTTCAG 1303
Db 908 GKGKADDDTDGTDKDDDKWDDKAKGTWGDATWAAATDWWWWGADADWWTWDAA 849

Qy 1304 GAGCTACTGTAAATCTGCAGATTTTCATCAACGCAATTTACAAACAAACACCTGCAC 1363
Db 848 ADDWADDDWADWAKWDDAWANGARTADRRDWDGRA-KRGGARKRRDRKADKRDA 790

Qy 1364 CCCTTACTCTCAGTAATGGTTTCTATGTCGAAGATCATGCTCAGCTTACAGTGA--- 1420
Db 789 DDRDDAATWTTTWTTRTDWKKKTDWTRWAADRTWDRDDDDDRDRAGTAGRKWRT 730

Qy 1421 ATCGATTACACAACTGGGGGTGTTCTCTCTGGGAATGGACGAGCTTCGTGAGTCT 1480
Db 729 WRRWRKRDTRDDADADDTAHDRRRRGGDAGAGKGTGRKRRDRATWDRTDW 670

Qy 1481 ATAAATCGTGCAGAAATCTCTAGCAATGCTCTATACACTGAAGCATATGGAT 1540
Db 669 ADAATTTTDTDDWDRRRKARRRRRTARAADWTTWAKWAKWDRKTRADRW 610

Qy 1541 TGAATCTTCTTCATCTGAAAGTGGTGGAGATTCCTTTATGT 1588
Db 609 DRWAADTWTDAKADRWAKARAWRRDRARAARRRRTTKGKTTT 562

RESULT 2
BJ390296 BJ390296 667 bp mRNA linear EST 08-MAR-2002
LOCUS Dictyostelium discoideum cDNA library, SF Dictyostelium
DEFINITION Dictyostelium cDNA clone dds21123 5', mRNA sequence.

ACCESSION BJ390296
VERSION BJ390296.1 GI:19301382
KEYWORDS EST.

SOURCE Dictyostelium discoideum.
ORGANISM Dictyostelium discoideum
REFERENCE 1 (bases 1 to 667)
AUTHORS Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.

Urushihara, H., Tanaka, Y., Kohara, Y. and Shin-i, T.
Full length cDNA of Dictyostelium discoideum at the slug stage
JOURNAL Unpublished (2002)
CONTACT: Tadasu Shin-1

Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.

FEATURES
Location/Qualifiers
1. 667
/organism="Dictyostelium discoideum"
/strain="AX4"
/db_xref="taxon:44689"
/clone="dds21123"
/clone_lib="Dictyostelium discoideum cDNA library, SF"
/sex="mat A"
/dev_stage="Slug stage"

BASE COUNT 318 a 89 g 198 t 5 others
ORIGIN

Query Match 1.5%; Score 44.6; DB 13; Length 667;
Best Local Similarity 50.2%; Pred. No. 0.5;
Matches 110; Conservative 0; Mismatches 109; Indels 0; Gaps 0;

Qy 931 GGAGCTATTACGTCCTGCTAGTACCCTAGTGGATAATGGCCCTACTCTTTATAAC 990
Db 257 GGAATTTTAAACGCTCACCAATGGTTCAATGGAATAATAACAACAATAATAAT 316

Qy 991 AATATCGCAATAATAAGGGGGCGCTATCTATATAGACGACCACTCCAAATTT 1050
Db 317 AATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAAT 376

Qy 1051 TCTGCCGACCGCCTGCTATTATTTTAAATGAAATATTTGTGACTAATGTACTACTGCA 1110
Db 377 AATAGCCACCAATAATAATAATAATGGAATAATAATAATAATAATAATAATAAT 436

Qy 1111 AATGTACCACTACGTCAGCTAATCCTCTAGAGAAAT 1149
Db 437 AATAATAGTAATAATAATAGTAATAATAATAATAATAGTAAT 475

RESULT 3
CNS04AEE/C

LOCUS Tetraodon nigroviridis genome survey sequence T7 end of clone
DEFINITION 095G24 of library G from Tetraodon nigroviridis, genomic survey
sequence.

ACCESSION AL281759
VERSION AL281759.1 GI:8020086
KEYWORDS GSS; genome survey sequence.
SOURCE Tetraodon nigroviridis.

ORGANISM Tetraodon nigroviridis

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontidae; Tetraodon.

REFERENCE 1 (bases 1 to 806)
AUTHORS Roest-Crolius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C.,
Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F.,
Saurin, W. and Weissbach, J.

TITLE Human gene number estimate provided by genome wide analysis using
Tetraodon nigroviridis DNA sequence

JOURNAL Unpublished
REFERENCE 2 (bases 1 to 806)
AUTHORS Roest-Crolius, H., Jaillon, O., Dasilva, C., Fizames, C., Fisher, C.,
Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and
Weissenbach, J.

TITLE Characterization and repeat analysis of the compact genome of the
freshwater pufferfish Tetraodon nigroviridis

JOURNAL Unpublished
REFERENCE 3 (bases 1 to 806)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (12-APR-2000)

COMMENT This sequence is a single read and was generated as part of a large


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/db_xref="taxon:99883"
/clone="221J14"
/clone_lib="G"
/note="Genoscope sequence ID : COAG221D507LP1-end : T7"
BASE COUNT      316 a   216 c   176 g   301 t      2 others
ORIGIN

Query Match      1.5%; Score 44; DB 17; Length 1011;
Best Local Similarity 52.1%; Pred. No. 0.82;
Matches 98; Conservative 0; Mismatches 90; Indels 0; Gaps 0;

QY 263 ATACACAAAAGAGGTTATTTATTGCAAAAAATCTCACCCCTGAAAGTGGTGGTGGCA 322
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 715 ATAAAAATCATAATGTAATTTATTTCCAGTGAACATTTCTCTGGAAGCAACACTGGGA 656
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 323 TTGGTTATGCGAGTCCCAATTCCTACCGTGGAGATTCTGTGATACATATGCTCTGTAA 382
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 655 TTAATTTTGAGAAGTATGATGATATCCCTGTGGAGGCTACTGGAACGAATGCCCATGCC 596
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 383 TCTTTGAAAATAAATACTTGTTCGACACCATTTACATCGAGTAATCCTAATCGAGCTGTTA 442
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 595 ACATTGAAGTGTAGTATATGCAATGCTTTTGAATGATTACTACTCAAAATTCAGGCTC 536
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 443 ATAAAA 450
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 535 TTAATAA 528

RESULT 6
BJ438828/c
LOCUS
DEFINITION      BJ438828 Dictyostelium discoideum cDNA library, linear EST 13-MAR-2002
                  dictyostelium cDNA clone ddv38115 3', mRNA sequence.
ACCESSION      BJ438828
VERSION        BJ438828.1 GI:19413550
KEYWORDS
SOURCE
ORGANISM
Dictyostelium discoideum.
Dictyostelium discoideum
Eukaryota; Mycetozoa; Dictyosteliida; Dictyostellium.
1 (bases 1 to 531)
Urushihara,H., Tanaka,Y., Kohara,Y. and Shin-i,T.
Full length cDNA of Dictyostelium discoideum at the vegetative
stage
Unpublished (2002)
Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
1..531
/organism="Dictyostelium discoideum"
/strain="AX4"
/db_xref="taxon:44689"
/clone="ddv38115"
/clone_lib="Dictyostelium discoideum cDNA library, VF"
/sex="mat A"
/dev_stage="Growth phase"
BASE COUNT      161 a   70 c   56 g   236 t      8 others
ORIGIN

Query Match      1.5%; Score 43.8; DB 13; Length 531;
Best Local Similarity 45.1%; Pred. No. 0.77;
Matches 153; Conservative 0; Mismatches 186; Indels 0; Gaps 0;

QY 258 TTTTGATACAAAAAGGATTTATTTTGGCAAAAATCTCACCCCTGAAAGTGGTGG 317
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 436 TTTTGATGATGATGATGATGATGCTGTCATATAGATGATGAAAAATATAGCAGTACAAG 377
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 318 TGGCATTTGGTTATGCGAGTCCCAATTCCTACCGTGGAGATTGCGTATACAATAGTCC 377
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```

2
3
4
5

LOCUS CENS0182P 1101 bp DNA linear GSS 26-JUL-1999
DEFINITION Drosophila melanogaster genome survey sequence SP6 end of BAC
BACN37D10 of DrosBAC library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
ACCESSION AL108811 GI:5629115
VERSION AL108811.1
KEYWORDS GSS.
SOURCE Drosophila melanogaster.
ORGANISM Drosophila melanogaster.
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 1101)
AUTHORS Direct Submission
TITLE Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
JOURNAL BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- web : www.genoscope.cns.fr)
COMMENT Determination of this BAC-end sequence was carried out as part of a
collaboration with the European Drosophila Genome Project (EDGP) -
http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC
library (Dros BAC) was made by Alain Billaud at CEPH (Centre
d'Etude du Polymorphisme Humain) with funding provided by a MRC
project grant. The DNA was prepared from embryos by Alain Bucheton
and Genevieve Payan. It has been constructed in the vector
pBelOBAC11.
FEATURES
Location/Qualifiers
source 1..1101
/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone="BACN37D10"
/clone_lib="DrosBAC"
/plasmid="pBelOBAC11"
/notes="end : SP6"
BASE COUNT 274 a 268 c 128 g 73 t 358 others
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Best Local Similarity 14.6%; Pred. No. 4.5;
Matches 51; Conservative 161; Mismatches 137; Indels 0; Gaps 0;
Qy 365 ATACAATAGGCTGTAATCTTTGAAATAATACTGTCGAGACCAATTTACATCGAGTA 424
||| : : : ||| :
Db 749 ATATWTDWATWATDKAATDTDAKRAAGRRKRDARTARDGGRRARTRRRAAAGGKRA 808
Qy 425 ATCTAATGACGCTGTTAATAAATAAGAGAGCGGAGCCATTCATGCTCAAAATCTTT 484
:
Db 809 RAGARRARAARADRDWDAAWAAAAAATAAATTTWRDRWDWDWDTRWDDDTTAA 868
Qy 485 ACATAAATCAATCATCATGCTGCGATTATGAGAAGCTTTTCTTATGTCGAGGAG 544
:
Db 869 WDDARARARRRRRRRRARRAARADDTDKRWADATTDKDTKTWTTDDDDWD 928
Qy 545 GAGCATTAGTACCGCTAATACCTTTGTTGAGCGAGATCAGTCTGTTTCTCTTTA 604
:
Db 929 KAKRDRWAADGAWKWRDARDWAATAKDDGWDKNGKRGKDKKRWKDKTG 988
Qy 605 TGGACACATCTGTATCAAACTATACAGAGAAAGGTGGCGCTATCTATCTGTGAA 664
:
Db 989 KKDDDDWDKWTWRDWWTTTKDWWDDGGRGRWTRKRNGAWWRADAWARDTDDGD 1048
Qy 665 CGAGCAATCTTTGAGAGTAATACTCGGATCTCTCTTTATCAATAA 713
:
Db 1049 TRTADKRRKRTDTRDGGDDWRKDKKRRDKKGGDKTKKDATWDDDD 1097
RESULT 13
BF298817
LOCUS BF298817 667 bp mRNA linear EST 04-MAY-2001
DEFINITION 021PG02 Pb cDNA #20, Charles Yowell and Jane Carlton Plasmodium
berghel cDNA 5', mRNA sequence.
ACCESSION BF298817
VERSION BF298817.1 GI:13952043

KEYWORDS Plasmodium berghel.
SOURCE Plasmodium berghel.
ORGANISM Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
REFERENCE 1 (bases 1 to 667)
AUTHORS Carlton,J.M.-R. and Dame,J.B.
TITLE The Plasmodium vivax and P. berghel gene sequence tag projects
JOURNAL Parasitol. Today (Regul. Ed.) 16 (10), 409 (2000)
COMMENT Contact: Dame JB
Department of Pathobiology, College of Veterinary Medicine
University of Florida
2015 SW 23rd Avenue, Bldg 1017, Gainesville, FL 32611-0880, USA
Tel: 352 392 4700
Fax: 352 392 9704
Email: damej@mail.vetmed.ufl.edu
Seq primer: T3
Location/Qualifiers
source 1..667
/organism="Plasmodium berghel"
/strain="ANKA clone 15cyl (clone of the ANKA 8417 HP clone
)"
/db_xref="taxon:5821"
/clone_lib="Pb cDNA #20, Charles Yowell and Jane Carlton"
/dev_stage="asynchronous blood stage"
/lab_host="Swiss white mice"
/notes="Vector: pBluescript II vector DNA, excised from
Lambda ZAP II.; Site_1: EcoRI; Site_2: XhoI; Total RNA was
extracted from asynchronous blood stage forms of the
cloned ANKA isolate of P. berghel grown in laboratory
Swiss white mice. Contaminating host white cells had
previously been removed using a novel biomagnetic bead
protocol (J. Carlton et al., manuscript in preparation).
PolyA+ RNA was extracted and reverse transcribed using an
oligo dt-XhoI primer. Second strand cDNA was prepared
using RNase H and DNA polymerase I. EcoR I adaptors were
ligated to the cDNA, and it was digested with XhoI.
Fragments were size selected, and those between 1-5 kb
ligated into EcoRI /XhoI digested vector."
BASE COUNT 339 a 49 c 70 g 209 t
ORIGIN
Query Match 1.4%; Score 41.2; DB 12; Length 667;
Best Local Similarity 48.3%; Pred. No. 4.4;
Matches 115; Conservative 0; Mismatches 123; Indels 0; Gaps 0;
Qy 263 ATACACAAAAGAGGATTTATTTTGCAGAAAATCTCACCCCTGGAAGTGGTGGCGGA 322
||| : : : ||| :
Db 149 ATGAAAAACATATGATATAGAAATGGAAGAGGATATAAACTGTAAAGCGCAATGATA 208
Qy 323 TTGCTTATGCGAGTCCCAATCTCTACCGTGGAGATTCGATACATAAGTCTCTCTAA 382
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Db 209 TTTTATTACAGTTAATATTTTGTAAATAATAATAGTAATAGTAATAGTATGATGAA 268
Qy 383 TCTTTGAAAATAATATCTTTGTCAGACCATTTACATCGAGTAATCTTAATCGACTGTA 442
||| : : : ||| :
Db 269 AAATAGAAAAAATATAGTACACAAAAACATAGAAAAATAGTATAATAAAGAAATG 328
Qy 443 ATAAAAAAGAGAGGCGGCGCATTCATGCTCAAAATCTTTTACATAAATCAATCA 500
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Db 329 ATAAAAAATAAAGATATATTTCTCTATTGAAGAAGAAATTTAAAAAGATTATTTCA 386
RESULT 14
BJ438184/c
LOCUS BJ438184 312 bp mRNA linear EST 13-MAR-2002
DEFINITION BJ438184 Dictyostelium discoideum cDNA library, VF Dictyostelium
discoideum cDNA clone dv36k13 3', mRNA sequence.
ACCESSION BJ438184
VERSION BJ438184.1 GI:19412906
KEYWORDS EST.
SOURCE Dictyostelium discoideum.
ORGANISM Dictyostelium discoideum.
Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.

```
REFERENCE 1 (bases 1 to 312)
AUTHORS Urushihara,H., Tanaka,Y., Kohara,Y. and Shin-I,T.
TITLE Full length cDNA of Dictyostelium discoideum at the vegetative
JOURNAL stage
COMMENT Unpublished (2002)
Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.
FEATURES
source
1..312
/organism="Dictyostelium discoideum"
/strain="AX4"
/db_xref="taxon:44689"
/clone="ddv3613"
/clone_lib="Dictyostelium discoideum cDNA library, VF"
/sex="mat A"
/dev_stage="Growth phase"
BASE COUNT 86 a 37 c 27 g 147 t 15 others
ORIGIN
Query Match 1.4%; Score 41; DB 13; Length 312;
Best Local Similarity 45.8%; Pred. No. 4;
Matches 116; Conservative 0; Mismatches 137; Indels 0; Gaps 0;
Qy 871 GATGTACAGGCAATCGGTAGGATCTTTTATAGTACATATCACAATAATATATGCG 930
||||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 269 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 210
Qy 931 GGAGCTATTTCCTGCTAGTACCTAGTGGGATATGGCCCTACCTACTTTTATAAAC 990
||||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 209 ATGATATTAATACCTCCCNATATAATAATAATAATAATATGNCNATAGCAATATGATACC 150
Qy 991 AATATCGCAATAATAAGGGGGCGCTATCTATATAGACGGAACCAACTCCAAATTT 1050
||||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 149 NATAATAATAATAACAATAGTAATACACTACNACTNCTAATAATAATAATAATAATGATAGT 90
Qy 1051 TCTGCGGACCGCATGCTATATTTTAAATGAAATATATGTCACCTAACTAAATGCA 1110
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Db 89 AATAATTCNAACTNCTAATAATAATAATAATAATAATAATAATAATAATAATAATGAT 30
Qy 1111 AATGTACCACTA 1123
|||
Db 29 GATAANGAAGTA 17

RESULT 15
BJ355703/c 415 bp mRNA linear EST 07-MAR-2002
DEFINITION BJ355703 Dictyostelium discoideum cDNA library, AF Dictyostelium
discoideum cDNA clone dda57022 3', mRNA sequence.
ACCESSION BJ355703
VERSION BJ355703.1 Gi:19255297
KEYWORDS EST.
SOURCE Dictyostelium discoideum.
ORGANISM Dictyostelium discoideum.
REFERENCE 1 (bases 1 to 415)
AUTHORS Urushihara,H., Tanaka,Y., Kohara,Y. and Shin-I,T.
TITLE Full length cDNA of Dictyostelium discoideum at the aggregation
JOURNAL stage
COMMENT Unpublished (2002)
Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.
FEATURES
source
1..415
/organism="Dictyostelium discoideum"
/strain="AX4"
/db_xref="taxon:44689"
/clone="dda57022"
/clone_lib="Dictyostelium discoideum cDNA library, AF"
/sex="mat A"
/dev_stage="Aggregation stage"
BASE COUNT 130 a 53 c 41 g 189 t 2 others
ORIGIN
Query Match 1.4%; Score 41; DB 13; Length 415;
Best Local Similarity 44.8%; Pred. No. 4.3;
Matches 152; Conservative 0; Mismatches 187; Indels 0; Gaps 0;
Qy 258 TTTTGATACACAAAAGAAGGTATTTATTTTGCAAAAATCTCACCCCTGAAAGTGGTGG 317
||||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 385 TTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 326
Qy 318 TCGGATTGGTTATGGAGTCCCAATTCCTACCGTGGAGATTCGTGATACATAATAGGTCC 377
||||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 325 TGGTCAAAATGATTAATACTACCAATATNAATAATAATAATAATAATAATAATAATA 266
Qy 378 TGTAACTTTGAAAATAATACTTTGTCAGACCATTTTACATCGAGTAATCCTAATGCGAGC 437
||||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 265 TGATACCAATAATAATAATAACAATAGTAATACTACTACTACTACTACTACTACTACTAA 206
Qy 438 TGTAAATAATAAGAGAGCGGAGCCATTCATCCTCAAAATCTTTACATAAATCATAA 497
||||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 205 TGATAGTAATAATTCAAACTNTACTAATAATAATAATAATAATAATAATAATAATAATA 146
Qy 498 TCATGATGTGGTCGGATTATGAGAACTTTTCTTTATCGGAGGAGGAGCCATTAGTAC 557
||||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 145 TAATGATCATTAATGAACTAATAATAGCGGATATGCTCTAAGTAGTAATGCAATAATAT 86
Qy 558 CGCTAATACCTTTGTTGAGCGGAGAAATCAGTCTTTGTTT 596
||||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 85 TAATAGTAGTGTGGTGGAGGTGTTACTCATCATTTTTT 47
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Search completed: February 4, 2003, 19:08:01
Job time : 3587 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: February 4, 2003, 15:52:32 ; Search time 7193 Seconds
(without alignments)
11725.279 Million cell updates/sec

Title: US-09-677-752-1
Perfect score: 2898
Sequence: 1 atgaaaaagcgtttttctt.....aaattgctgcgattcttag 2898

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
Searched: 2054640 seqs, 14551402878 residues
Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 20000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 3: gb_in.*
- 4: gb_om.*
- 5: gb_ov.*
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- 11: gb_sts.*
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- 37: em_htg_vrt.*
- 38: em_sy.*
- 39: em_htgo_hum.*
- 40: em_htgo_mus.*
- 41: em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2821.2	97.3	2895	6	AX155928 Sequence
2	2821.2	97.3	2895	6	AX361778 Sequence
c 3	2818	97.2	14177	1	AE001360 Chlamydia
4	2777.8	95.9	2934	6	AX155940 Sequence
5	2777.8	95.9	2934	6	AX361790 Sequence
c 6	1599.4	55.2	14482	1	AE002293 Chlamydia
c 7	1190.6	41.1	1634	6	AX338273 Sequence
8	136.4	4.7	2805	6	AX349485 Sequence
c 9	136.4	4.7	10746	1	AE002190 Chlamydia
10	136.4	4.7	12083	1	AE001631 Chlamydia
11	136.4	4.7	300650	1	AF002546 Chlamydia
c 12	124.2	4.3	10236	1	AE002189 Chlamydia
13	88	3.0	2817	6	AX349483 Sequence
14	56.6	2.0	14482	1	AE002293 Chlamydia
15	48.4	1.7	2949	6	AX155927 Sequence
16	48.4	1.7	2949	6	AX361777 Sequence
17	48.4	1.7	3021	6	AX155939 Sequence
18	48.4	1.7	3021	6	AX361789 Sequence
c 19	48.2	1.7	107289	2	AC116923 Dictyoste
c 20	47.6	1.6	160759	2	AC117082 Dictyoste
c 21	47.2	1.6	298283	3	AE003782 Drosophil
22	47	1.6	12838	1	AE002338 Chlamydia
23	46	1.6	35276	2	AC115611 Dictyoste
24	46	1.6	86904	2	AC117177 Dictyoste
25	45.8	1.6	3353	3	AF482386 Dictyoste
26	45.2	1.6	1941	6	AX156073 Sequence
27	45.2	1.6	1941	6	AX361923 Sequence
28	45.2	1.6	14177	1	AE001360 Chlamydia
29	45	1.6	193924	2	AC095241 Rattus no
c 30	44.8	1.5	40156	2	AC100852 Homo sapi
c 31	44.8	1.5	161245	9	AC009158 Homo sapi
32	44.8	1.5	189250	9	AC093511 Homo sapi
33	44.6	1.5	105470	2	AC116306 Dictyoste
34	44.2	1.5	4000	1	AF242295 Bacillus
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ALIGNMENTS

RESULT 1
AX155928
LOCUS
DEFINITION Sequence 171 from Patent WO0140474.
ACCESSION AX155928
VERSION AX155928.1 GI:14537033
KEYWORDS Chlamydia sp.
SOURCE Chlamydia sp.
ORGANISM Chlamydia sp.
REFERENCE 1 (bases 1 to 2895)
AUTHORS Probst,P., Bhatia,A., Skeiky,Y.A., Fling,S.P. and Scholler,J.
TITLE Compounds and methods for treatment and diagnosis of chlamydial infection
JOURNAL Patent: WO 0140474-A 171 07-JUN-2001;

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RESULT 3

AE001360/c

LOCUS

DEFINITION Chlamydia trachomatis section 87 of 87 of the complete genome.

ACCESSION AE001360 AE001273

14177 bp

DNA

linear

BCT 30-OCT-2000

VERSION	AE001360.1	GI:3329342	
KEYWORDS	Chlamydia trachomatis.		
SOURCE	Chlamydia trachomatis.		
ORGANISM	Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.		
REFERENCE	1 (bases 1 to 14177)		
AUTHORS	Stephens,R.S., Kalman,S., Lammel,C.J., Fan,J., Marathe,R., Aravind,L., Mitchell,W.P., Olinger,L., Tatusov,R.L., Zhao,Q., Koonin,E.V. and Davis,R.W.		
TITLE	Genome sequence of an obligate intracellular pathogen of humans: Chlamydia trachomatis		
JOURNAL	Science 282 (5389), 754-759 (1998)		
MEDLINE	99000809		
REFERENCE	9784136		
AUTHORS	2 (bases 1 to 14177)		
TITLE	Kalman,S., Mitchell,W., Marathe,R., Lammel,C., Fan,J., Hymen,R.W., Olinger,L., Grimwood,J., Davis,R.W. and Stephens,R.S.		
JOURNAL	Comparative genomes of Chlamydia pneumoniae and C. trachomatis		
MEDLINE	Nat. Genet. 21 (4), 385-389 (1999)		
REFERENCE	99206606		
AUTHORS	3 (bases 1 to 14177)		
TITLE	Stephens,R.S., Kalman,S., Lammel,C.J., Fan,J., Marathe,R., Aravind,L., Mitchell,W.P., Olinger,L., Tatusov,R.L., Zhao,Q., Koonin,E.V. and Davis,R.W.		
JOURNAL	Direct Submission		
FEATURES	Submitted (20-MAY-1998) Program in Infectious Diseases, University of California, 235 Warren Hall, Berkeley, CA 94720-7360, USA		
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DB 3027 GGTGTGTTCTCTTGGGAATGGAGCAGTCTGAGTTCCTATAAAAAATGGTGCAGGAAT 2968
QY 1501 TCTGCTAGCAATGCTCTTATAACACTGAAGCATATTGATTTGAATCTTTTCTTCCATTTCTG 1560
DB 2967 TCTGCTAGCAATGCTCTTATAACACTGAAGCATATTGATTTGAATCTTTTCTTCCATTTCTG 2908
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RESULT 4	AX155940	2934 bp	DNA	linear	PAT 22-JUN-2001
LOCUS	AX155940	Sequence 183 from Patent WO0140474.			
DEFINITION	AX155940	1 (bases 1 to 2934)			
ACCESSION	AX155940	Probst,P., Bhatia,A., Skeiky,Y.A., Fling,S.P. and Scholler,J.			
VERSION	AX155940.1	Compounds and methods for treatment and diagnosis of chlamydia infection			
KEYWORDS	AX155940.1	GI:14537039			
SOURCE	Chlamydia sp.				
ORGANISM	Chlamydia sp.				
REFERENCE	Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.				
AUTHORS	1 (bases 1 to 2934)				
TITLE	Probst,P., Bhatia,A., Skeiky,Y.A., Fling,S.P. and Scholler,J.				
JOURNAL	Compounds and methods for treatment and diagnosis of chlamydia infection				
FEATURES	Patent: WO 0140474-A 183 07-JUN-2001;				
source	CORIXA CORPORATION (US)				
BASE COUNT	Location/Qualifiers				
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	875 a 645 c 575 g 839 t				
Query Match	95.98;	Score 2777.8;	DB 6;	Length 2934;	
Best Local Similarity	98.68;	Pred. No. 0;			
Matches 2813;	Conservative 0;	Mismatches 37;	Indels 3;	Gaps 1;	
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Qy	106	ACGAAGAGTGGCTATCAAAATAAAATTTAGTTGACAGGAGACACTCAAAATCTCACTAAC	165		
Db	145	ACGAAGAGTGGCTATCAAAATAAAATTTAGTTGACAGGAGACACTCAAAATCTCACTAAC	204		
Qy	166	TGCTATCTCGATACCTACCGCTACATACACTGGCTATTTCTACAAAAAATCCCAATGAGGA	225		
Db	205	TGCTATCTCGATAACCTACCGCTACATACACTGGCTATTTCTACAAAAAATCCCAATGAGGA	264		
Qy	226	GCTGCTGTCAATTAACAGATTTACCTAAGCTTTTTTGATACACAAAAAAGAGGTATTAT	285		
Db	265	GCTGCTGTCAATTAACAGATTTACCTAAGCTTTTTTGATACACAAAAAAGAGGTATTAT	324		
Qy	286	TTTGCAAAAATCTACCCCTGAAAGTGGTGGCGATTTGGTTATGGGAGTCCCAATTCT	345		
Db	325	TTTGCAAAAATCTACCCCTGAAAGTGGTGGCGATTTGGTTATGGGAGTCCCAATTCT	384		
Qy	346	CCTACCGTGGAGATTGCTGATACAAATAGGTCCTGTAATCTTTGAAAAATAATCTGTTGC	405		
Db	385	CCTACCGTGGAGATTGCTGATACAAATAGGTCCTGTAATCTTTGAAAAATAATCTGTTGC	444		
Qy	406	AGACCATTTACATCGAGTATCTCTTAATGCAGCTGTTTAAATAAAGAGAGCGGAGCC	465		
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Qy	466	ATTTCATGCTCAAAATCTTTACATAAATCAATAATCATGATGCTGTCGATTTATCAAGAAC	525		
Db	502	ATTTCATGCTCAAAATCTTTACATAAATCAATAATCATGATGCTGTCGATTTATCAAGAAC	561		
Qy	526	TTTTCTTTATGCCAGGAGGAGCCATTAGTACCGCTAATACCTTTTGTGTGAGCGAGAAT	585		
Db	562	TTTTCTTTATGCCAGGAGGAGCCATTAGTACCGCTAATACCTTTTGTGTGAGCGAGAAT	621		
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Qy	646	GGCGCTATCTATGCTGAACGACAAATCTTTTGAGAGTAATAACTCGCATCTCTCTTT	705		
Db	682	GGCGCTATCTATGCTGAACGACAAATCTTTTGAGAGTAATAACTCGCATCTCTCTTT	741		
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Db 982 CTGTAGTTACCTAGTGATATGSCCTACCTACTTTTATAAACAATATCGCCAAATAT 1041
QY |||||
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Db 1042 AAGGGGGCGCTATCTATATAGACGGAACAGCAACTCCAAAATTTCTGCCGACGCCAT 1101
QY |||||
QY 1066 GCTATATTTTAAATGAAAAATATGTGACTAATGTAACTAATGCAAAATGGTACCACTAGC 1125
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QY |||||
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Db 1222 TTAGGAGCAGGAGTAGCCAAAATTTAATTTTATGATCCATTGAAGTTAGCAATGCA 1281
QY |||||
QY 1246 GGGGTCTGTGCTCTCAATAGGAAGCTGATCAAAACAGGCTGTGTAGTATTTTCAGA 1305
Db 1282 GGGGTCTGTGCTCTCAATAGGAAGCTGATCAAAACAGGCTGTGTAGTATTTTCAGA 1341
QY |||||
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QY |||||
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|||

Db 1822 ATAGATTTTTCGGGACTAAATGTCCCTCATATGATGTCGAAGGACTTTTGGACTTTGGGC 1881
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Db 1942 GCCAATAGATTCCATAGAACCTTACTACTAACATGCTTCCTGCCGGTATGTTCCCTAGC 2001
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|||

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Db 3138 ACAATTTACTGATCCGAAAAGCTAATCAGTTTTCATAGAACTTTATTAACGTGGCTC 3079
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QY 2005 GGGATATGCTCTTGCACAGAAAAGCTTAAAAATAGTGCAGAACTGCACACTAGTGAT 2064
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Qy	2545	GGAGCCTATCCGGAAGCTTTTCTACAAAGACTCCTTTGATCAATATGCTAGTCCCTATT	2604		
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Qy	2605	GGAGTTAAAGGTAGCTTTATCAATGCTACCAAGAGACTCAAGCCTGGACTGTAGAATTG	2664		
Db	2418	GGAGTAAAGGTAGCTTCATGAATGCCACCATTAGACTCAGGCTGGACTGTAGAGCTT	2359		
Qy	2665	GCATACCAACCCGTTTCTGTATAGACAAGAACCGAGGATCGCGACCCAGCTCCTAGCCAGT	2724		
Db	2358	GCTTACCAACCTGTTCTTTACAGACAAGAACTAGTATCTACCCAACTACTCGCTGGT	2299		
Qy	2725	AAGGGTATTTGGTTGGTAGTGGGAAGCCCTTCATCGCGGTCAATGCCATGTCTATAAATC	2784		
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Qy	2785	TCACAGCAACACAAACCTTTTGAGTTGGTTAACTTCTCAATTCAGTATCATGGATTCTAC	2844		
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Qy	2845	TCCTCTCAACCTTCTCTGAATATATCTCAATGGGAAATTTGCTCTGCGATTCTTA	2897		
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RESULT 7					
AX338273/c		1634 bp DNA linear PAT 09-JAN-2002			
LOCUS		AX338273			
DEFINITION		Sequence 43 from Patent WO0181379.			
ACCESSION		AX338273			
VERSION		AX338273.1 GI:18128808			
KEYWORDS		Chlamydia trachomatis.			
SOURCE		Chlamydia trachomatis.			
ORGANISM		Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.			
REFERENCE		1 Bhatia, A., Probst, P. and Stromberg, E.J.			
AUTHORS		Compounds and methods for treatment and diagnosis of chlamydia			
TITLE		infection			
JOURNAL		Patent: WO 0181379-A 43 01-NOV-2001;			
FEATURES		CORIXA CORPORATION (US)			
source		Location/Qualifiers			
BASE COUNT		1.1634			
ORIGIN		/organism="Chlamydia trachomatis"			
		/db_xref="taxon:813"			
		485 a 293 c 356 g 500 t			
Query Match 41.1%; Score 1190.6; DB 6; Length 1634;					
Best Local Similarity 99.0%; Pred. No. 3.4e-264;					
Matches 1209; Conservative 0; Mismatches 9; Indels 3; Gaps 1;					
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Qy	61	GTTCCCTCTAGAACTTTCTTTATGCCCAACTCAGTTCAGATCCTACGAAAGAGTCGCTA	120		
Db	1158	GTTCCCTCTAGAACTTTCTTTATGCCCAACTCAGTTCAGATCCTACGAAAGAGTCGCTA	1099		
Qy	121	TCAAATAAAATTAGTTTGGACAGGAGACACTCACAAATCTCACTAACTGCTATCTCGATAAC	180		
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TITLE McClarty,G., Salzberg,S.L., Eisen,J. and Fraser,C.M.
JOURNAL Genome sequences of Chlamydia trachomatis MoPn and Chlamydia
MEDLINE pneumoniae AR39
PUBMED Nucleic Acids Res. 28 (6), 1397-1406 (2000)
REFERENCE 20150255
AUTHORS 10684935

2 (bases 1 to 10746)
Read,T.D., Brunham,R.C., Shen,C., Gill,S.R., Heigelberg,J.F.,
White,O., Hickey,E.K., Peterson,J., Umayam,L.A., Utterback,T.,
Berry,K., Bass,S., Linher,K., Weidman,J., Khouri,H., Craven,B.,
Bowman,C., Dodson,R., Gwinn,M., Nelson,W., DeBoy,R., Kolonay,J.,
McClarty,G., Salzberg,S.L., Eisen,J. and Fraser,C.M.
Direct Submission

TITLE Submitted (01-MAR-2000) The Institute for Genomic Research, 9712
JOURNAL Medical Center Dr, Rockville, MD 20850, USA
COMMENT On Jun 1, 2000 this sequence version replaced gi:7189209.
FEATURES Location/Qualifiers

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RECORDS	
SOURCE	Chlamydoiphila pneumoniae CWL029.
ORGANISM	Chlamydoiphila pneumoniae CWL029
	Bacteria; Chlamydiales; Chlamydiaceae; Chlamydoiphila.
REFERENCE	1 (bases 1 to 12083)
AUTHORS	Kalman,S., Mitchell,W., Marathe,R., Lammel,C., Fan,J., Hyman,R.W., Olinger,L., Grimwood,J., Davis,R.W. and Stephens,R.S.
TITLE	Comparative genomes of Chlamydia pneumoniae and C. trachomatis
JOURNAL	Nat. Genet. 21 (4), 385-389 (1999)
MEDLINE	99206506
PUBLISHED	10192388
REFERENCE	2 (bases 1 to 12083)
AUTHORS	Kalman,S., Mitchell,W., Marathe,R., Lammel,C., Fan,J., Olinger,L., Grimwood,J., Davis,R.W. and Stephens,R.S.
TITLE	Direct Submission
JOURNAL	Submitted (01-DEC-1998) Program in Infectious Diseases, University of California, 235 Earl Warren Hall, Berkeley, CA 94720, USA
FEATURES	Location/Qualifiers
SOURCE	1..12083

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REFERENCE	Bacteria; Chlamydiales; Chlamydiaceae; Chlamydophila.		
AUTHORS	Shirai,M., Hirakawa,H., Ouchi,K., Tabuchi,M., Kishi,F., Kimoto,M., Takeuchi,A., Nishida,J., Shibata,K., Fujinaga,R., Yoneda,H., Matsushima,H., Tanaka,C., Furukawa,S., Miura,K., Nakazawa,A., Ishii,K., Shiba,T., Hattori,M., Kuhara,S. and Nakazawa,T. Comparison of outer membrane protein genes omp and pmp in the whole genome sequences of Chlamydia pneumoniae isolates from Japan and the United States J. Infect. Dis. 181 Suppl 3, S524-S527 (2000)		
JOURNAL MEDLINE REFERENCE	20298986		
AUTHORS	Shirai,M., Hirakawa,H., Kimoto,M., Tabuchi,M., Kishi,F., Ouchi,K., Shiba,T., Ishii,K., Hattori,M., Kuhara,S. and Nakazawa,T. Comparison of whole genome sequences of Chlamydia pneumoniae J138 from Japan and CWL029 from USA Nucleic Acids Res. 28 (12), 2311-2314 (2000)		
TITLE	3 (bases 1 to 300650)		
JOURNAL MEDLINE REFERENCE	20330349		
AUTHORS	Shirai,M.		
TITLE	Direct Submission		
JOURNAL	Submitted (04-JUL-2000) Mutsunori Shirai, Yamaguchi University School of Medicine, Department of Microbiology; 1-1-1 Minamikoogushi, Ube, Yamaguchi 755-8505, Japan (E-mail:mshirai@epo.cc.yamaguchi-u.ac.jp, Tel:81-836-22-2227, Fax:81-836-22-2415)		
COMMENT	On or before Sep 15, 2000 this sequence version replaced gi:6172290, gi:6172292, gi:6172294, gi:6172296, gi:6172326, gi:6172328, gi:6172330, gi:6172332, gi:6172334, gi:6172336, gi:6172338, gi:6172382, gi:6172384, gi:6172386, gi:6172388, gi:6172390, gi:6172392, gi:6172394, gi:6174666, gi:6174668, gi:6635174, gi:6635176, gi:6635178, gi:6635180, gi:8547433, gi:8547438, gi:8978640.		
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VERSION AE002189.2 GI:8163402
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ORGANISM Chlamydomophila pneumoniae AR39.
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AUTHORS Read,T.D., Brunham,R.C., Shen,C., Gill,S.R., Heidelberg,J.F.,
White,O., Hickey,E.K., Peterson,J., Umayam,L.A., Utterback,T.,
Berry,K., Bass,S., Linher,K., Weidman,J., Khouri,H., Craven,B.,
Bowman,C., Dodson,R., Gwinn,M., Nelson,W., DeBoy,J., Kolonay,J.,
McClarty,G., Salzberg,S.L., Eisen,J. and Fraser,C.M.
TITLE Genome sequences of Chlamydia trachomatis MoPn and Chlamydia
pneumoniae AR39
JOURNAL Nucleic Acids Res. 28 (6), 1397-1406 (2000)
MEDLINE 20150295
PUBMED 10684935
REFERENCE 2 (bases 1 to 10236)
AUTHORS Read,T.D., Brunham,R.C., Shen,C., Gill,S.R., Heidelberg,J.F.,
White,O., Hickey,E.K., Peterson,J., Umayam,L.A., Utterback,T.,
Berry,K., Bass,S., Linher,K., Weidman,J., Khouri,H., Craven,B.,
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McClarty,G., Salzberg,S.L., Eisen,J. and Fraser,C.M.
TITLE Direct Submission
JOURNAL Submitted (01-MAR-2000) The Institute for Genomic Research, 9712
Medical Center Dr, Rockville, MD 20850, USA
COMMENT On Jun 1, 2000 this sequence version replaced gi:7189205.
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gene

gene

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VERSION	AE002293.1	GI:7190298	
KEYWORDS			
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ORGANISM	Chlamydia muridarum		
REFERENCE	Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.		
AUTHORS	Read,T.D., Brunham,R., Shen,C., Gill,S.R., Heidelberg,J.F., White,O., Hickey,E.K., Peterson,J., Umayam,L.A., Utterback,T., Berry,K., Bass,S., Linher,K., Weidman,J., Khouri,H., Craven,B., Bowman,C., Dodson,R., Gwinn,M., Nelson,W., DeBoy,R., Kolonay,J., McClarty,G., Salzberg,S.L., Eisen,J. and Fraser,C.M.		
TITLE	Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39		
JOURNAL	Nucleic Acids Res.	28 (6), 1397-1406 (2000)	
MEDLINE	20150255		
PUBMED	10684935		
REFERENCE	2 (bases 1 to 14482)		
AUTHORS	Read,T.D., Brunham,R., Shen,C., Gill,S.R., Heidelberg,J.F., White,O., Hickey,E.K., Peterson,J., Umayam,L.A., Utterback,T., Berry,K., Bass,S., Linher,K., Weidman,J., Khouri,H., Craven,B., Bowman,C., Dodson,R., Gwinn,M., Nelson,W., DeBoy,R., Kolonay,J., McClarty,G., Salzberg,S.L., Eisen,J. and Fraser,C.M.		
TITLE	Direct Submission		
JOURNAL	Submitted (01-MAR-2000) The Institute for Genomic Research, 9711 Medical Center Dr, Rockville, MD 20850, USA		
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QY 949 GTAGTTACCCFAGTGGATAATGCGCCCTACCTACTTTATATAACAATATCGCCAATAATAAG 1008
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ACCESSION AX155927
VERSION   AX155927.1 GI:14537032
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           Chlamydia sp.
ORGANISM  Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
REFERENCE 1 (bases 1 to 2949)
AUTHORS   Probst,P., Bhatia,A., Skeiky,Y.A., Fling,S.P. and Scholler,J.
TITLE      Compounds and methods for treatment and diagnosis of chlamydial
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JOURNAL   Patent: WO 0140474-A 170 07-JUN-2001;
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GenCore version 5.1.1.3
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OM protein - protein search, using sw model

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285.245 Million cell updates/sec

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Perfect score: 5086

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Scoring table: BLOSUM62

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Searched: 129505 seqs, 22169297 residues

Total number of hits satisfying chosen parameters: 129505

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Post-processing: Minimum Match 0%

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Listing first 45 summaries

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4	647	12.7	982	10	US-09-841-132-176
5	647	12.7	1006	10	US-09-841-132-190
6	645	12.7	925	10	US-09-452-380-4
7	645	12.7	936	10	US-09-452-380-3
8	636	12.5	926	9	US-10-023-437-57
9	605.5	11.9	715	10	US-09-841-132-321
10	595	11.7	1016	12	US-10-007-693-95
11	583	11.5	978	12	US-10-007-693-65
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13	531	10.4	839	9	US-10-023-437-23
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18	459.5	9.0	866	10	US-09-841-132-189
19	456.5	9.0	931	10	US-09-779-081-2

20	398.5	7.8	1752	10	US-09-841-132-180	Sequence 180, App
21	395	7.8	1751	10	US-09-841-132-445	Sequence 445, App
22	395	7.8	1751	10	US-09-841-132-594	Sequence 594, App
23	388.5	7.6	679	9	US-10-023-437-53	Sequence 53, Appl
24	386.5	7.6	1530	12	US-09-841-132-178	Sequence 178, App
25	386	7.6	1531	12	US-10-007-693-98	Sequence 98, Appl
26	371.5	7.3	715	10	US-09-841-132-329	Sequence 329, App
27	365	7.2	848	10	US-09-841-132-192	Sequence 192, App
28	363	7.1	1776	10	US-09-841-132-179	Sequence 179, App
29	345.5	6.8	948	10	US-09-841-132-194	Sequence 194, App
30	342	6.7	1770	10	US-09-841-132-444	Sequence 444, App
31	340	6.7	646	10	US-09-841-132-317	Sequence 317, App
32	320.5	6.3	691	10	US-09-841-132-313	Sequence 313, App
33	278.5	5.5	631	10	US-09-841-132-325	Sequence 325, App
34	278	5.5	871	10	US-09-886-468-21	Sequence 21, Appl
35	277.5	5.5	439	10	US-09-841-132-524	Sequence 524, App
36	246.5	4.8	514	10	US-09-886-468-23	Sequence 23, Appl
37	246.5	4.8	619	10	US-09-841-132-309	Sequence 309, App
38	235	4.6	700	10	US-09-841-132-345	Sequence 345, App
39	234	4.6	375	10	US-09-886-468-20	Sequence 20, Appl
40	221.5	4.4	821	10	US-09-841-132-195	Sequence 195, App
41	220.5	4.3	654	10	US-09-841-132-341	Sequence 341, App
42	215	4.2	778	10	US-09-841-132-193	Sequence 193, App
43	213	4.2	469	10	US-09-886-468-18	Sequence 18, Appl
44	205	4.0	683	10	US-09-841-132-357	Sequence 357, App
45	188.5	3.7	583	10	US-09-841-132-353	Sequence 353, App

ALIGNMENTS

RESULT 1

US-09-841-132-177
; Sequence 177, Application US/09841132
; Patent No. US20020061848A1
; GENERAL INFORMATION:
; APPLICANT: Bhatia, Ajay
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Probst, Peter
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
; FILE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
; FILE REFERENCE: 210121.469C8
; CURRENT APPLICATION NUMBER: US/09/841,132
; CURRENT FILING DATE: 2001-04-23
; NUMBER OF SEQ ID NOS: 599
; SOFTWARE: FastSeq for Windows Version 3.0/4.0
; SEQ ID NO 177
; LENGTH: 964
; TYPE: PRT
; ORGANISM: Chlamydia
US-09-841-132-177

Query Match					98.2%;	Score 4994.5;	DB 10;	Length 964;
Best Local Similarity					98.4%;	Pred. No. 0;		
Matches 950;					Conservative	7;	Mismatches	7;
							Indels	1;
							Gaps	1;
Qy	1	MKKAF	FFFLIGNSLGLAREVPSRFLMPNSVDPDTKESLSNKISLTGDTNLTNCYLDN	60				
Db	1	MKKAF	FFFLIGNSLGLAREVPSRFLMPNSVDPDTKESLSNKISLTGDTNLTNCYLDN	60				
Qy	61	LVYLAI	LQKTNEGAAVTIDYLSFFDTQKEGIYFAKNLTPESGAIGYASPSPTVEI	120				
Db	61	LVYLAI	LQKTNEGAAVTIDYLSFFDTQKEGIYFAKNLTPESGAIGYASPSPTVEI	120				
Qy	121	RDITGP	VFENNCCRPFTSSNPAAVNKIREGGAIHQALYINHNHDVVGPMKFSYVR	180				
Db	121	RDITGP	VFENNCCRPFTSSNPAAVNKIREGGAIHQALYINHNHDVVGPMKFSYVR	179				
Qy	181	GGAIST	ANTFVYSENSQCFLEMDNICIQNTAGKGAIYAGTSNFESNCDLFFINNAC	240				
Db	180	GGAIST	ANTFVYSENSQCFLEMDNICIQNTAGKGAIYAGTSNFESNCDLFFINNAC	239				
Qy	241	CAGGAI	FPICSLTGNRGNIVNRCFNKVTASSEADGGAIKVTTTLDVYGNRGRIF	300				

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|||||
Db 240 CAGGAIFSPICSLGNRGNIYFVNNRCFKNYETASSEASDGGAIKVTTRLDVTGNRGRIF 299
Qy 301 FSDNITKNYGAIVAPVVTLDNGPTTFINNANKGGAIIYIDGTSNKSISADRHAIIFN 360
Db 300 FSDNITKNYGAIVAPVVTLDNGPTTFINNANKGGAIIYIDGTSNKSISADRHAIIFN 359
Qy 361 ENIVNTVNTANGTSTSANPPRRNAITVASSSGEILLGAGSSQNLIIFYDPIEVSNAQSVS 420
Db 360 ENIVNTVNTANGTSTSANPPRRNAITVASSSGEILLGAGSSQNLIIFYDPIEVSNAQSVS 419
Qy 421 FNKEADQTSVVFSGATVNSADFHORNLOTKTTPAPLTLNSGFLCIEDHAQLTIVNRFTQTG 480
Db 420 FNKEADQTSVVFSGATVNSADFHORNLOTKTTPAPLTLNSGFLCIEDHAQLTIVNRFTQTG 479
Qy 481 GVVSILGNCAVLSCKYKNGAGNSASNASITLKHIGLNLSSILKSGAEIPLLLWVEPTNNSNY 540
Db 480 GVVSILGNCAVLSCKYKNGAGNSASNASITLKHIGLNLSSILKSGAEIPLLLWVEPTNNSNY 539
Qy 541 TADTAATFSLSDVKLSLIDDDYGNPSYESTDLTHALSSQPMLSISEASDNQLRSDMDPSG 600
Db 540 TADTAATFSLSDVKLSLIDDDYGNPSYESTDLTHALSSQPMLSISEASDNQLRSDMDPSG 599
Qy 601 LNVPYHGWGLTWGWAQTOPEPASSATITDPQKANRFRHTLLLTWLPAGYVPSPKHRS 660
Db 600 LNVPYHGWGLTWGWAQTOPEPASSATITDPQKANRFRHTLLLTWLPAGYVPSPKHRS 659
Qy 661 PLIANTLWGNMMLLATESLKNKSAELTPSDHPFWGITGGGLGMVYQDPRENHPGFHMRSSG 720
Db 660 PLIANTLWGNMMLLATESLKNKSAELTPSGHPFWGITGGGLGMVYQDPRENHPGFHMRSSG 719
Qy 721 YSAGMIAGOTHFSLKFSOTYTKLNERYAKNNVSKNYSQOGEMLFSLQEGFLTCLKVGL 780
Db 720 YSAGMIAGOTHFSLKFSOTYTKLNERYAKNNVSKNYSQOGEMLFSLQEGFLTCLKVGL 779
Qy 781 YSAGDHCHHFTYTOGENTLQSGTFRSQTMGGAVFDDLPMPKFGSTHILTAFLGALGIYS 840
Db 780 YSAGDHCHHFTYTOGENTLQSGTFRSQTMGGAVFDDLPMPKFGSTHILTAFLGALGIYS 839
Qy 841 SLSHFTVEGAYPRFSFKTPLINVLPIGVKGSFNMNATORPOAWTVELAYQPVLYRQEPG 900
Db 840 SLSHFTVEGAYPRFSFKTPLINVLPIGVKGSFNMNATORPOAWTVELAYQPVLYRQEPG 899
Qy 901 IATOLLASKGIWFGSGSPSSRHMSYKISQOTQPLSWLTLHFQYHGYSSTFCNLYNGE 960
Db 900 IATOLLASKGIWFGSGSPSSRHMSYKISQOTQPLSWLTLHFQYHGYSSTFCNLYNGE 959
Qy 961 IALRF 965
Db 960 IALRF 964
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RESULT 2

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US-09-841-132-191
; Sequence 191, Application US/09841132
; Patent No. US20020061848A1
; GENERAL INFORMATION:
; APPLICANT: Bhatia, Ajay
; APPLICANT: Sreiky, Yasir A.W.
; APPLICANT: Probst, Peter
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
; FILE REFERENCE: 210121.469CB
; CURRENT APPLICATION NUMBER: US/09/841.132
; CURRENT FILING DATE: 2001-04-23
; NUMBER OF SEQ ID NOS: 599
; SOFTWARE: FastSeq for Windows Version 3.0/4.0
; SEQ ID NO 191
; LENGTH: 977
; TYPE: PRT
; ORGANISM: Chlamydia
US-09-841-132-191
```

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Query Match 96.7%; Score 4919.5; DB 10; Length 977;
Best Local Similarity 98.4%; Pred. No. 0;
Matches 935; Conservative 7; Mismatches 7; Indels 1; Gaps 1;
Qy 16 GLAREVPSRFLPMNSVDPDPKESLSNKSISLTGDTNLTNCYLDNLRYLAILOKTPNEG 75
Db 29 GLAREVPSRFLPMNSVDPDPKESLSNKSISLTGDTNLTNCYLDNLRYLAILOKTPNEG 88
Qy 76 AAVTITDYLSPFDQKEGIYFAKNLTIPESGGAIGAYSPNSPTVEIRDTIGVPIFENNPTCC 135
Db 89 AAVTITDYLSPFDQKEGIYFAKNLTIPESGGAIGAYSPNSPTVEIRDTIGVPIFENNPTCC 148
Qy 136 RPFTSSNPNAVNKIREGGAIHAQNLXINHNHVVGMKFNFSYVYRGGAISTANTFVYVSEN 195
Db 149 RLEWTRNPYAA-DKIREGGAIHAQNLXINHNHVVGMKFNFSYVYRGGAISTANTFVYVSEN 207
Qy 196 QSCFLFMDNTICIQNTAGKGAIIYAGTNSFESNNCDLFFINNACCAGGAIFFSPICSLTG 255
Db 208 QSCFLFMDNTICIQNTAGKGAIIYAGTNSFESNNCDLFFINNACCAGGAIFFSPICSLTG 267
Qy 256 NRGNIYFNNRCFKNVETASSEASDGGAIKVTTRLDVTGNRGRIFFSDNITKNYGGAIYA 315
Db 268 NRGNIYFNNRCFKNVETASSEASDGGAIKVTTRLDVTGNRGRIFFSDNITKNYGGAIYA 327
Qy 316 PVVTLVDNGPTTFINNANKGGAIIYIDGTSNKSISADRHAIIFENINIVTNTANGTST 375
Db 328 PVVTLVDNGPTTFINNANKGGAIIYIDGTSNKSISADRHAIIFENINIVTNTANGTST 387
Qy 376 SANPPRRNAITVASSSGEILLGAGSSQNLIIFYDPIEVSNAQSVSFNKEADQTSVVFSG 435
Db 388 SANPPRRNAITVASSSGEILLGAGSSQNLIIFYDPIEVSNAQSVSFNKEADQTSVVFSG 447
Qy 436 ATVNSADFHORNLOTKTTPAPLTLNSGFLCIEDHAQLTIVNRFTQGVVYSLNGAVLSYCK 495
Db 448 ATVNSADFHORNLOTKTTPAPLTLNSGFLCIEDHAQLTIVNRFTQGVVYSLNGAVLSYCK 507
Qy 496 NGAGNSASNASITLKHIGLNLSSILKSGAEIPLLLWVEPTNNSNYTADTAATFSLSDVKL 555
Db 508 NGTGDASNASITLKHIGLNLSSILKSGAEIPLLLWVEPTNNSNYTADTAATFSLSDVKL 567
Qy 556 SLIDDYGNPSYESTDLTHALSSQPMLSISEASDNQLRSDMDPSGLNVPYHGWGLTWG 615
Db 568 SLIDDYGNPSYESTDLTHALSSQPMLSISEASDNQLRSDMDPSGLNVPYHGWGLTWG 627
Qy 616 WAKTQDEPASAATITDPQKANRFRHTLLLTWLPAGYVPSPKHRSPLIANTLWGNMLIAT 675
Db 628 WAKTQDEPASAATITDPQKANRFRHTLLLTWLPAGYVPSPKHRSPLIANTLWGNMLIAT 687
Qy 676 ESLKNSAELTPSDHPFWGITGGGLGMVYQDPRENHPGFHMRSSGYSGAGMIAGOTHTFSL 735
Db 688 ESLKNSAELTPSDHPFWGITGGGLGMVYQDPRENHPGFHMRSSGYSGAGMIAGOTHTFSL 747
Qy 736 KFSQTYTKLNERYAKNNVSKNYSQOGEMLFSLQEGFLTCLKVGLYSYGDHCHHFTYQG 795
Db 748 KFSQTYTKLNERYAKNNVSKNYSQOGEMLFSLQEGFLTCLKVGLYSYGDHCHHFTYQG 807
Qy 796 ENLTSQGTFRSQTMGGAVFDDLPMPKFGSTHILTAFLGALGIYSSLSHSHTFEGAYPRSF 855
Db 808 ENLTSQGTFRSQTMGGAVFDDLPMPKFGSTHILTAFLGALGIYSSLSHSHTFEGAYPRSF 867
Qy 856 STKTPLINVLPIGVKGSFNMNATORPOAWTVELAYQPVLYRQEPGIATQLLASKGIWFGS 915
Db 868 STKTPLINVLPIGVKGSFNMNATORPOAWTVELAYQPVLYRQEPGIATQLLASKGIWFGS 927
Qy 916 GSPSSRHMSYKISQOTQPLSWLTLHFQYHGYSSTFCNLYNGEIALRF 965
Db 928 GSPSSRHMSYKISQOTQPLSWLTLHFQYHGYSSTFCNLYNGEIALRF 977
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RESULT 3

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US-09-886-468-22
; Sequence 22, Application US/09886468
; Patent No. US20020037293A1
```

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; GENERAL INFORMATION:
; APPLICANT: Aventis Pasteur Limited
; TITLE OF INVENTION: Chlamydia antigens and corresponding DNA fragments and uses there
; FILE REFERENCE: 77813-5
; CURRENT APPLICATION NUMBER: US/09/886,468
; CURRENT FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: 60/113,280
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: 60/113,281
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: 60/113,282
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: 60/113,283
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: 60/113,284
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: 60/113,285
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: 60/113,385
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: 60/114,050
; PRIOR FILING DATE: 1998-12-28
; PRIOR APPLICATION NUMBER: 60/114,056
; PRIOR FILING DATE: 1998-12-28
; PRIOR APPLICATION NUMBER: 60/114,057
; PRIOR FILING DATE: 1998-12-28
; PRIOR APPLICATION NUMBER: 60/114,058
; PRIOR FILING DATE: 1998-12-28
; PRIOR APPLICATION NUMBER: 60/114,059
; PRIOR FILING DATE: 1998-12-28
; PRIOR APPLICATION NUMBER: 60/114,061
; PRIOR FILING DATE: 1998-12-28
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 22
; LENGTH: 963
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
US-09-886-468-22

Query Match          19.5%; Score 989.5; DB 10; Length 963;
Best Local Similarity 30.0%; Pred. No. 3.9e-68;
Matches 304; Conservative 146; Mismatches 416; Indels 149; Gaps 34;

QY 9 LIGNSLGLA-----REVPSRIFLMP-----NSVPDPKTESLSNKISLTDTHNL----- 54
DB 30 LSGNEVPLNASCOMSKKDISAHTSPSFLNVTPEPLVSSFRPSNLLNGFGHDITQDITI 89
QY 55 -----NCYLD-NRLYLAILQKTPNEGAATITDLSFFDTQKEGIYFAKNLTPESGGAI 108
DB 90 TGNINSVIDYNYHY-----EDGGILACKNL--FISENKGNLSPERNSSHSGGAL 138
QY 109 GYASPNSPVETRDITGPIVFENNCCRPFTSSNP-----AAVKNIREGGAHA 158
DB 139 -----YSVRE-----C--WISKKNYSFISNAASLATTTTSGFGGAHA 175
QY 159 QNLYINHNDVYVGMKNSYVRGGAISTANTFVWSENQSCFLFMDNICIOTNTACKGAI 218
DB 176 LDSYITNLNGEQFLDYSKNGGAIYGVCSLITDNLGPIVKKNQILEDSSP--GGGI 233
QY 219 YAGTNSFESNCDLFFINNACAGGAIFSPICSLTGNRGNIYFYNRCFKNVTASSEA 278
DB 234 FCRAVN-IERNYONIQINDNASGOGVYVFLPLGVIISSNKEIIEISNHSASSINTASGL 292
QY 279 SDGGAIKVTRLDVTGN-RGRIFFSNDITKNYGGAIY-----APVTVLDNGPTFIINI 332
DB 293 YPGGGIMCTSLSHENNPKGLIF--NNKTAALSGGVYTRDLSSSKITV-----RTAFINNS 346
QY 333 ANKKGAIYIDG-----TNSKISADRHALIFENIVTNVANGTSTANPRRRAITVA 388
DB 347 ATSGGALLNLSIGTGPQNFLLSADYGDILFNNTI-----TSSSPQPGYRNAL-YA 397
QY 389 SSSGBEILLGAGSSQNLIFYDPIEVSNAGVS-VSFNKEADQTCGVVFSGATVNSADFQNRN 447
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DB 398 AFGINLKLARGQYKILFYDPDHDHQTTPDPIVNFVPEHHLGTVLFSGINVDSNATNPLN 457
QY 448 LQTKPAPLTLNSGFLCIEDHAQLVNRFTQGTGGVVSNGAVLSYKNGAGNSASNASI 507
DB 458 FLSKFSNSRSLRGLVAIEDRAAIKCTLSQGTGILRLGNAALIR--TKGPG-----SSI 510
QY 508 TLKHIGLNLSSLSLKSGAEIPLLVNPTNNNSNYTADTAATFSLSDVKLSLIDDYGNSPYE 567
DB 511 NFENATAINLPSILOSEASAPKFWIYPTLTGSTYSEDSTSTIISLG-PLTFINDENENPYD 569
QY 568 STDLTALSSQPMLSISEASDNQLRSDMDDFSGLVN-----PHYGWOGLTWGAKTQD 621
DB 570 SLDL-----SEPRKDIPLPPLPPRCCKKIDTNSNLIVEAMNLDEHYGQGIWSPYMET-- 622
QY 622 PEPASSATITDPQKANRPHRTLLLTWLPAGYVPSPKHSRSLIANTILW-----GNML 673
DB 623 ---TTTTSTVPEQNTNHRQLYVDWTPVGYRPNRPERHGEFTANTLWQSAYNALLGIRIL 679
QY 674 ATESLKN---SAELTPSDHPFMGITGGGLGMVYQDPRENHPGFHMRSSGYSAGMIA--G 728
DB 680 PPQNLKEHDLASLQ-----GLGLLNQHNREGRKGRFNHTGYAATTSAKTA 727
QY 729 QHTFSLKFSQYTKLNERYAKNNVSSKNYSCQEMFLSQEGFLTLKLVLGYISYGDHN- 787
DB 728 ARHSFSLGFAQMFKTRERQSPSTTSSHNYFAGLRFDLSLLFRDFTSTGLSLGYSYGDHMH 787
QY 788 -CHHEFTQGENLTSGTFRSQTMGCAVFDLPKMPFGSTHIL-TAPFGLGALGIYSSLSHF 845
DB 788 LCH--YTEILKGGSKAFFNNHTVLAS--DCTFLPARITRTLELQFPFISAILRCSQASF 843
QY 846 TEVGAYPRSFSTKTPLINVLVPIGVKGSFMMATQRPQAWTVELAYOPVLYROEPIATOL 905
DB 844 QETGDHIRKFKHPKPLDLSLSPIGFRSEWKTSHHPLMLWTTEISVTVPLYRKNPENFTTL 903
QY 906 LASKGIWFGSGSPSRSHAMYSKISQOTQPLSWLTLHFQYHGYSSSTFCNYLNGE 960
DB 904 LISNGTWTQTATPVSNSVAAKIKNTSOLFSSRVTLSDYSQAQVSSSTVGQYLKAE 958

RESULT 4
US-09-841-132-176
; Sequence 176, Application US/09841132
; Patent No. US20020061848A1
; GENERAL INFORMATION:
; APPLICANT: Bhatia, Ajay
; APPLICANT: Skeely, Yasir A.W.
; APPLICANT: Probst, Peter
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
; FILE REFERENCE: 210121.469C8
; CURRENT APPLICATION NUMBER: US/09/841.132
; CURRENT FILING DATE: 2001-04-23
; NUMBER OF SEQ ID NOS: 599
; SOFTWARE: FastSeq for Windows Version 3.0/4.0
; SEQ ID NO 176
; LENGTH: 982
; TYPE: PRT
; ORGANISM: Chlamydia
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(982)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-841-132-176

Query Match          12.7%; Score 647; DB 10; Length 982;
Best Local Similarity 25.4%; Pred. No. 1.1e-41;
Matches 257; Conservative 156; Mismatches 388; Indels 212; Gaps 43;

QY 39 SLSNKSISTGDTNLTNLCYLNRLYLAILOKTPNEGAATITDLSFFDTQKEGIYFAK 98
DB 54 NLLGSFTVLGRHSILT---FENIR-----TSTNGAALS-----NSAADGLF--- 91
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Qy 122 DTIGPVIFENN-----TCCRPPTSSNPAAVNKIREGGAIHAQNLVYINHNHVDVVGFMK 174
Db 114 SAADKNLLFNDPFRSLIISCPSSLSTPGQALSKV-----GNLSLTCGNSQII-FTQ 164
Qy 175 NFSYVRGAISTANTFVYSENQSCFLFMDNICIQNTAGKGAIYA-GTNSFESNCDL 233
Db 165 NFSDDNGGVINTKN-FLLSGTSQFASFSRN---QAFTKQGGVYVYATGTTIENSPIGVIS 220
Qy 234 FFINNACCAGAIIPS-PICSLUTGNGRNIVFYNNRCFNVTASSEADSGGAIKVTT--R 289
Db 221 FSQNLARGSGGALYSTDCNSITDN-FQVIFDGSAMEAAQ-----AQGGAICTTTDKT 273
Qy 290 LDVTGNGRIFPFSNITKNYGGAIYAPVTVLDVNGPFFYFNNIANKK-----GGAIYIDG 344
Db 274 VLTGCK-NLSFTNTALTGGAISGLKVISAGGPTLFQSNISGSGAGQGGGAINIAS 332
Qy 345 TSNKISADRHAIFINENIVNTVNTANGTSTSANPPRNATVASSGEILLGAGSSONL 404
Db 333 AGEALATSATSGDITFNNQVNTN-----GSTST-----RNAINIIDTAKVTSIRAATGQSI 382
Qy 405 IFYDPIEVSAGVSVS-----FNKEADOTGVSVEGSGATVNSAD-PHORNLOTKTP 453
Db 383 YFYDPI--TNPQTAASDTLNLNADANSEIEYGAIVFSGEKUSPTEKAIAANVTSTIR 440
Qy 454 APTLSNGFELCIEDHAOLTVNRFTQTGGVYSLGNGAVLSCYKNGAGNSASNASITLKHIG 513
Db 441 QPAVLARGDLVLRGVTVTFKDLTQSPGSRILMDG-----GTTLSAKEANLSLNGLA 492
Qy 514 LNLSSILKGAIEPLLVVEPTNNNSNTTADTAATFSLSDVKLSLIDYGNPSYESTDLTH 573
Db 493 VNLSL-----DGTNKAALKTEAADKNISLSGT-IALIDTEG-SFYENHNLS 538
Qy 574 ALSOPMLSTSEASDN-OLRSDDDMFSLGNVP--HYCWOGLWTWGWAKTODPEPASATI 630
Db 539 A-STYPLLELTAGANTITLIGALSTLTLOBPETHYGTQGNWQLSWAN-----ATSSKI 591
Qy 631 TDPOKANRHFRTLLTLWLPAGYVPSPKHRSPLIANTLWGNMMLLATESLKNSAELTPSDHP 690
Db 592 GS-----INWTRTGYIPSPERKSNLPLNSLWGN-FIDIRSIINQLIETKSSGEP 638
Qy 691 F-----WGITGGGLGMVYQDPREHNHPGFMHRSSGYSAGMTAGQTHTSLKFSQTYTKLNE 746
Db 639 FERELW---LSGIANFFYRDSMPTRHGFHISGGYALGITATTPAEDQLTFA--FCQLFA 693
Qy 747 RYAKNNVSSKN-----YSCOGEMLFSLQEGFL-----LTKLVGL---- 780
Db 694 R-DRNHITGKNHGDTYCASLYFHHTGLEFDI-ANFLGKATRAPWVLSEISQIIPLSFDA 751
Qy 781 ---YSYGDHNCHEHYTQGENLTSQGTFRSOTMGGAFFDLPMPKFPFGSTHIL--TAPFLGA 835
Db 752 KFSYLHTDNHMKTYTT--DNSIIKGSWRNDAFCADLGASLPF-VISVPYLLKEVEPEVKV 808
Qy 836 LGIYSSLSHTEVCAYPRSESTKPLNLVLPVIGVKSEFNNAQORPOAATVELAYQVPL- 894
Db 809 QYIIAHOOQFYERHAEGRAFN-KSELINVEIPIGVT---FEROSKSEKGYDTJLTLMYILD 864
Qy 895 -YROEPGIATQLLASKGIWFGSGSPSSRHAMSYKISQOTQPLSWLTHFYQHYGYSSTF 953
Db 865 AYRNPACQTSLIASDANWYATGNLARQGFVSRAAHNFQVNPMEIFGQF-AFEVRSSS 923
Qy 954 CNYLNGEIALRUF 965
Db 924 RNY-NTNLGSKF 934

RESULT 8

US-10-023-437-57
; Sequence 57, Application US/10023437
; Publication No. US20020183272A1
; GENERAL INFORMATION:
; APPLICANT: JOHNSTON, STEPHEN A.
; APPLICANT: STEMKE-HALE, KATHERINE
; APPLICANT: SYKES, KATHRYN F.

; APPLICANT: KALTENBOECK, BERNHARD
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR VACCINATION COMPRISING NUCLEIC AC
; TITLE OF INVENTION: AND/OR POLYPEPTIDE SEQUENCES OF CHLAMYDIA
; FILE REFERENCE: UTSID:7360S
; CURRENT APPLICATION NUMBER: US/10/023,437
; CURRENT FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: 60/225,839
; PRIOR FILING DATE: 2000-12-15
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 57
; LENGTH: 926
; TYPE: PRT
; ORGANISM: Chlamydia psittaci
US-10-023-437-57

Query Match 12.5%; Score 636; DB 9; Length 926;
Best Local Similarity 24.0%; Pred. No. 7.3e-41;
Matches 241; Conservative 157; Mismatches 365; Indels 240; Gaps 41;

Qy 41 SNKISLTGDTNHL--TNCYLDNLRYILAILQKTPNEGA-----AVTITDY--L 84
Db 82 ADNLTFKGNHNSUSITNA-----NAGANPAGINNVNADKLTITLDFSKL 125
Qy 85 SFEDTORQEGYIFAKNLTPESGGAIGYASPNSPPTVEIRDITGPIVFENNTCCRPFTSSNP 144
Db 126 SFRECPSSLVNTGKG-AMKSGGALNANNAS-----ILFDQN-----YSAEN-- 166
Qy 145 AAVNKIREGGAIHAQNLVYINHNHVDVGMKFNFSYVRGAISTANTFVYSENQSCFLFMDN 204
Db 167 -----GGAISKAFSLTGSSEKISFTTNTSTAKGGAIAATAIAHLSDNQGTIRFSGN 218
Qy 205 ICIOVTAGTGGAIYAGTSSNSFESNCDLFPINNACC-----AGGAFSPICSLUTGNGRN 259
Db 219 TAVNS-----GGAVYSEASMTIAGNN-HVAFSNNAVSGSSDCCGALH---CSKTGSAPT 269
Qy 260 IVFYNNRCFNKVFETASSEASDGGAIKVTTRLDVTGNGRIFPFSNITKNYGGAIYAPVVT 319
Db 270 LTIRDNKV-----LIFEENTSSAKGAIYTDKLI 298
Qy 320 LVDNGPYTFNN---IANKKGAIYIDGTSNKSISADRHAIIFNENIVNTVNTANGTSTS 376
Db 299 LTSGGPTAFITNNKVTATPKGGAIGIAANGECSLTAEPHGDITFDNNLMATQDNAT----- 353
Qy 377 ANPPRRNAIVASSSGEILLGAGSSONLIFYDPIEV--SNAGSVSYSENK-BADQF--GSV 432
Db 354 ---IKRNAINEGCKFPVNLRAASGKTIISYDPTIVEGNADLLTLNKAEGDKTYNGRII 410
Qy 433 FSGATVNS-----ADFHORNLOTKTPAPLTLSNGFLCIEDHAOLTVNRFTQGTGVVSLGN 487
Db 411 FSGEKLTREEQAANVAD---NLKTTFTQPTITLAAGELVLRSGVEAEKTVVQTAGSLILMD 466
Qy 488 GAVLSCYKNGAGNSASNASITLKHIGNLSSI-----LKSAGAEIPLW-----VEP 533
Db 467 A-----GTKUSAKTEDATLTNLAINPNTLDGKKFAVVDAAAGKNVTLSSGAIGVIDP 518
Qy 534 TNN--SNNYTADYAAATFSLSDVKLSLIDYGNPSYESTDL--THALSQPMLSISEASDNQ 590
Db 519 TGKFEYENHKLNDTLA---LGGIQLS-----GKGSVTTTNPSPHV----- 555
Qy 591 LRSDMDDFSGNLNPHYGYWQGLWTWGWAKTODPEPASATITDPOKANRHFRTLLTLWLP 650
Db 556 -----GVAETHYGYQGNWSVSVKVDNNSDKPT-----QTAIFTWNKT 592
Qy 651 GYVPSPKHRSPLIANTLWGNMMLLATESLKNSAELTPSD--HPFWGITGGGLGMVYQDPR 708
Db 593 GYVNPERRAPVLNLSLWGS-FIDLRSIQDVLERSVDSIILETRKRLVWSGIGNFPHKDRN 651
Qy 709 ENHPGFHMRSSGYSAGMIAGOTH--TFSLKFSQTYTKLNERYAKNNVSS----- 755
Db 652 AENKFRHISGIVLGATTNTSREDSLSVAFQCQLFAKDKDYLVSKNANVYAGSVYQHV 711
Qy 756 -----KNYSCQGEMLFSLQEGFLTLTLVLGLYSYGDHNCHEHYTQGENLTSQGT 803

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Db 712 SKFDDLTRFLNGPNTCCSG---FSKEIPFIPLDAQI--TYCHTANNMTTSYTDYDEV--KGS 765
QY 804 FRSQTMGGGAVFDPLMKPFGSTHILT-APFLGALGIYSSLSHTEVGAYPRFSFKTPLI 862
Db 766 WNDTILGLTSTSVPIPVFSSTFDSYAPFAKLQVVIYAHODDFKEPTTEGRVFES--SDLL 824
QY 863 NVLPVIGVGSFPMNATQRPQAWTVELAYQPVLYROBPGIATQALLASKGIWFGSGSPSRH 922
Db 825 NVSPVIGIKFELKSYGER--SAYDLILMYPDVYRHNPCSMCTGLAINDVSWLTATNLAQ 883
QY 923 AMSYKISQOTQPLSWTLHFQYHGFSSTFCNY---LNGETA 962
Db 884 AFIVRAGNHIALTSGVEMFSQF--GPELRSSRNYNVDLGAKVA 925

RESULT 9
US-09-841-132-321
; Sequence 321, Application US/09841132
; Patent No. US20020061848A1
; GENERAL INFORMATION:
; APPLICANT: Bhatia, Ajay
; APPLICANT: Skeiky, Ysair A.W.
; APPLICANT: Probst, Peter
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
; FILE REFERENCE: 210121.469C8
; CURRENT APPLICATION NUMBER: US/09/841,132
; CURRENT FILING DATE: 2001-04-23
; NUMBER OF SEQ ID NOS: 599
; SOFTWARE: FastSeq for Windows Version 3.0/4.0
; SEQ ID NO 321
; LENGTH: 715
; TYPE: PRN
; ORGANISM: Chlamydia trachomatis
US-09-841-132-321

Query Match 11.9%; Score 605.5; DB 10; Length 715;
Best Local Similarity 27.2%; Pred. No. 1.1e-38;
Matches 208; Conservative 120; Mismatches 277; Indels 159; Gaps 30;
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QY 302 SDNITKNYGGAIYA-PV-----VTLVDNGPTVFIN-NIANKKGAIYIDGTSNS 348
Db 11 SDNFQLSQGGCGFAIPIGQAMAIAGQIKLPTVHIGTAPFLGLGVVDNNGGARQVRVGS 70
QY 349 KISADRHAIIFNENIVNTVNTANGTSTSANPPRRAITVASSSGEILLGAGSQNLIFVD 408
Db 71 APAASLG--ISTGDVITAVDGA-----PINSATAMADALNG-----HH 106
QY 409 PIEVSNAGVSVSFNKEA--DQTSVVFSGATVNSADF-----HORNLOTKT----- 452
Db 107 PGDV-----ISVTWQKSGGTRTGNTWL--AEGPPAEFCRYPSHWRPLDRTLGMKEHNYI 160
QY 453 -PAPITLNGFLCIEDHAQLTVNR--FTQT--GGVYSLGNGAVLSCYKNGAGNSASNASIT 508
Db 161 KEAPTTLKFGTLAIEDDAELEIFNIPFTQNPFTSLLALSGATLTVGKHG-----KLN 212
QY 509 LKHIGLNLSSILKSGAEIPLLWVEFTN-NSNNYTADT--AATFSL-----DVKLSLDD 560
Db 213 ITNLGVILPILILEKGSPPCIRVNPQDMTQNTGTQTPSTSSISTPMIIFNGRLSIVDE 272
QY 561 YGNSPYESTDLPHALSSQPMLSISEASDNLRSDD--DMDFSLGNVPHYVGWGLWTGWA 617
Db 273 NYESYDSDMLSRGAEQILSIIETNDQGLDSNWQSSLTLSLPPHYGLOGLWTPNWI 332
QY 618 KT-----QDPEPASSATITDPOKANR-----638
Db 333 TTTTYITLNNSSAPTSAFSAIEQKKTSETFTPSNTTASIPNIKASAGSGSGSASNSGE 392
QY 639 ---FHTLLLTWLPAGYVSPKRPRLTANTL---WGNMLLATESLKSNAELTPSDHPFW 692
Db 393 VTITKHTLVNAPVGYIVDPRIIRGDLTANSLVSHGRNMTMLGRSLL-----PDNSWF 445
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QY 693 GITGGLGMVYQDPRENHPGFHMRSSGYSGAMIA--GOTHTFSLKFSQTYTKLNERYAK 750
Db 446 ALQGAATTLTKQOKRLSYHGYSASKGTVSSQASGAHGKFLLSFSOSSDKMEKEIN 505
QY 751 NVVSKNY---SCQGEMLFSLOEGFLTLKLVG--LYSYGDHNCHEHYTOGENLTSQGTFR 805
Db 506 NFLSSRYLSLALCFEHPMPD-----RIALGAAACNYGTHNMRSPY--GTRKSKGKRF 557
QY 806 SOTMGAVFFDL---PMKPFPGSTHILTAPFLGALGIYSSLSHTEVGAYPRFSFKTPL 861
Db 558 STTLGASLRCELRDSMLR-----SIMLTPFAQALFSRTEPASIRESGDLARLFTLEQAH 612
QY 862 INVLPVIGVGSFPMNATQRPQAWTVELAYQPVLYROBPGIATQALLASKGIWFGSGSPSR 921
Db 613 TAVVSPIGIKGAYSSDTWPTLSWEMELAYQPTLYWKRLPLNTLLIQNNSSWTTTNTPLAK 672
QY 922 HAMYSKISQOTQPLSWTLHFQYHGFSSTFCNYLNGEIALRF 965
Db 673 HSF-YGRGSHSLKFLSHLKLAFANYQAEVATSTVSHVINGAGALVF 715

RESULT 10
US-10-007-693-95
; Sequence 95, Application US/10007693
; Patent No. US20020146776A1
; GENERAL INFORMATION:
; APPLICANT: Bhatia, Ajay
; APPLICANT: Probst, Peter
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR TREATMENT
; TITLE OF INVENTION: AND DIAGNOSIS OF CHLAMYDIAL INFECTION
; FILE REFERENCE: 210121.515C2
; CURRENT APPLICATION NUMBER: US/10/007,693
; CURRENT FILING DATE: 2001-12-05
; NUMBER OF SEQ ID NOS: 157
; SEQ ID NO 95
; LENGTH: 1016
; TYPE: PRN
; ORGANISM: Chlamydia trachomatis serovar D
US-10-007-693-95

Query Match 11.7%; Score 595; DB 12; Length 1016;
Best Local Similarity 25.4%; Pred. No. 1.2e-37;
Matches 261; Conservative 149; Mismatches 404; Indels 214; Gaps 49;
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QY 42 NKISLTGDTHTNLT-----NCYLDNLRYLAILQKTPNEGAATITDYSFFDTQEGIFY 96
Db 69 DNLTTIGQNHFLSTDSOGPVLQNYAFISA-----GETLTKDFSS-----LMF 112
QY 97 AKNLTPESGGAGYASPNSTVEIRDITGPVIFENNT-----CCRP 137
Db 113 SKNVSCGEGMI-----SGKTVSISGA-GEVIFWDSNVGYSPLSIVPASTPTPPAPAPAP 166
QY 138 FTSSNPNAVNKIREGGAIHAQONLYINHNHDVYVPMKNFYSYVYRGGAI StantonFVYSENQS 197
Db 167 AASSLSLPTSDARKGSIFSIVET-----SLEISGVKKGVWF-----DNNAG 207
QY 198 CF--LPMDNICQTWTACKGGAIYAGTNSFESNCD---LFFINNACCAGAIISPCTS 252
Db 208 NFGTVFRGN---SNNNAGSGGS--GSATTPSTFVKCKGKVSFTDNVASCQGGVYKGTVL 263
QY 253 LTGNRGNTVFNRCFKNVETASSEASD-----GGA1-KVTTRLDVTGNRGRIFFSD 303
Db 264 FDNEGGIFFRGNTAYDDLGLLAATSRONTETGGGGVVCSPDSDSVKFEKNKGSIYFDY 323
QY 304 NITKNYGGAIYAPVTVLVDNGPTYFINNIANKGAIY---IDGTSNS-----KISAD 353
Db 324 NFAKRGGSILTKPELSVADDSVWFSSNNTAEKGGGAIYAPTIDISTNGSILFERNRAE 383
QY 354 RHAIIFNE-----NIVNTVNA-----NGTSTANPPRRAITVASSSGEILLGAGSQ 402
Db 384 GGAICVSEASSGSTGNLTLSADGDIVFSGNMTSDRPGERSAARILSDGTVSLNAGLS 443
QY 403 NLIFDYDPIEVSN--AGVS-----VSFKEADQGTGVVFSGATVNSADPHQ--RN 447
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: PRIOR APPLICATION NUMBER: 60/113,280
: PRIOR FILING DATE: 1998-12-23
: PRIOR APPLICATION NUMBER: 60/113,281
: PRIOR FILING DATE: 1998-12-23
: PRIOR APPLICATION NUMBER: 60/113,282
: PRIOR FILING DATE: 1998-12-23
: PRIOR APPLICATION NUMBER: 60/113,283
: PRIOR FILING DATE: 1998-12-23
: PRIOR APPLICATION NUMBER: 60/113,284
: PRIOR FILING DATE: 1998-12-23
: PRIOR APPLICATION NUMBER: 60/113,285
: PRIOR FILING DATE: 1998-12-23
: PRIOR APPLICATION NUMBER: 60/113,385
: PRIOR FILING DATE: 1998-12-23
: PRIOR APPLICATION NUMBER: 60/114,050
: PRIOR FILING DATE: 1998-12-28
: PRIOR APPLICATION NUMBER: 60/114,056
: PRIOR FILING DATE: 1998-12-28
: PRIOR APPLICATION NUMBER: 60/114,057
: PRIOR FILING DATE: 1998-12-28
: PRIOR APPLICATION NUMBER: 60/114,058
: PRIOR FILING DATE: 1998-12-28
: PRIOR APPLICATION NUMBER: 60/114,059
: PRIOR FILING DATE: 1998-12-28
: PRIOR APPLICATION NUMBER: 60/114,061
: PRIOR FILING DATE: 1998-12-28
: NUMBER OF SEQ ID NOS: 26
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 19
: LENGTH: 922
: TYPE: prt
: ORGANISM: Chlamydia pneumoniae
US-09-886-468-19

```

Query Match	11.2%;	Score 569.5;	DB 10;	Length 922;
Best Local Similarity	24.5%;	Pred. No. 1e-35;		
Matches 236;	Conservative 151;	Mismatches 354;	Indels 221;	Gaps 45;
QY	45	SLTGDTNLTNCLYLDNLRILIAILQKTPNEGAATITDYLSEFFDTQREGIYF---AKNLT 101		
DB		: : : : : : : : : : : : : : : : : : : : : : : : :		
QY	57	SLTGDV-SISN---VDN-----SALNK-----ACPNVTSGSVTFAGNHGGLFYNISSGTT 103		
DB		: : : : : : : : : : : : : : : : : : : : : : : : :		
QY	102	PESGGAICYASPNPTVEIRDITGVIFENNTCCRP-----FTSSNPAANAANKIRE 152		
DB		: : : : : : : : : : : : : : : : : : : : : : : : :		
QY	104	KE--GAV-----LCCODPOATARFSGFTSLFIQSPGDIKE 137		
DB		: : : : : : : : : : : : : : : : : : : : : : : : :		
QY	153	GGATHAONLYINHHDVVGMKNSYVRGGAISTANTFVSGENOSCFLEFMDNICIQTNWA 212		
DB		: : : : : : : : : : : : : : : : : : : : : : : : :		
QY	138	QGCLYSKNALMLLNYYVRFEQNSKTKGGAISGANTVIGN-----YDSVSFYQNA 190		
DB		: : : : : : : : : : : : : : : : : : : : : : : : :		
QY	213	GKGAIFYAGTSNPESNNCDLFFNNAC--CAGGAIFSPICSLTGNRGNIYFNNR--CF 268		
DB		: : : : : : : : : : : : : : : : : : : : : : : : :		
QY	191	TFGGAIHSSGQLAVNQAEIRFAQNTAKNGSGALYSD-----GDIDQNAVYLF 242		
DB		: : : : : : : : : : : : : : : : : : : : : : : : :		
QY	269	KNVTASEASDGAIKVTRLDVTGNRGR---IFFSDN-----TKNY---GAGIYAPV 317		
DB		: : : : : : : : : : : : : : : : : : : : : : : : :		
QY	243	RENEALTATGKGAV---CCLPTSGSSTPVPVTFSDNKQLVPERNHSIMGGGAIYARK 299		
DB		: : : : : : : : : : : : : : : : : : : : : : : : :		
QY	318	VTLVDNGPTFINNI---ANNKGAIYIDGTSNKSISADRHAIIFNENIVNTNANGT 373		
DB		: : : : : : : : : : : : : : : : : : : : : : : : :		
QY	300	LSISSGGPTFINNISYANSQNLGALTAIDPGBEISAEKGTITF-----QGN 348		
DB		: : : : : : : : : : : : : : : : : : : : : : : : :		
QY	374	STSANPPRRNAITVASSSGEILLGAGSSQNLIFYDPTEVSNAGYSVSFN-----KEADOT 428		
DB		: : : : : : : : : : : : : : : : : : : : : : : : :		
QY	349	RTSL--PFLNGIHLQNAKFLQARNGYSIEFDPT--TSEADSGTQLNINGDPPKNEYT 405		
DB		: : : : : : : : : : : : : : : : : : : : : : : : :		
QY	429	GSVVFGATVNSADFHORNLOTKTPAPLTLNSGFLCHIEDHAQLTVNRFTQTGG---VYSL 485		
DB		: : : : : : : : : : : : : : : : : : : : : : : : :		
QY	406	GTILFSGEKSILAND--PRDPKSTIPQNVNLSAGYLVIKEGAETVSVKFTQSPGSHLVLDL 463		
DB		: : : : : : : : : : : : : : : : : : : : : : : : :		
QY	486	GNGAVLSCYKNGAGNSASNAISITLKHGLNLSLILKSGAEIPLLWPEPTNNSNYTDATA 545		
DB		: : : : : : : : : : : : : : : : : : : : : : : : :		
QY	464	GTKLI-----ASKEDIAITGLAIDSLSSSSTA-----VTKANTANK----- 502		
DB		: : : : : : : : : : : : : : : : : : : : : : : : :		

QY	546	ATFSLSDVKLSLIDDDYGN	SPYESTDLTHALSSQPM	LSEISASDNQLRSDMD	DFSGLNVPH	6005
Db	503	-QISYTD-SIELISPTGNA-YEDLR	MNRNS-QTFPLLSLEPCAGG	SVTVTADGFLPVS-PH	557	
QY	606	YGWGLWTGWAKTODPEPASSATITD	PQANRPHRTLLLTWLPAGYVP	SPKHSPLIAN	665	
Db	558	YGFQGNKWLATWGTGN-----	KVGEF-----	WDKYNKPRPEKEGNLVPN	598	
QY	666	TLWGN-----MLLATSLK	KNASBELTPSDHPFWGITGG	GLGMVYQDPRENHPGFHMRS	719	
Db	599	ILWGNADVRSIMQVQETHASSLQ---	TDRLGW---IDGIGNFHV	SVASSEDNIRYRHNSG	652	
QY	720	GY--SAGMIAGQTHFSLKESQTYTK	LNERYAKNNVSKNYS	COGEMFLFSLOGBFLLLTKL	777	
Db	653	GYVLSVNNETPKHYTSMATFSOLF	SR-DKDYAVSNNEYRMY--	LGSVLYO-----YTTSL	704	
QY	778	VGLYSYGDHN-----	CHHEYTQGENLTSQGTFR-----	805		
Db	705	GNIFRYASRNPVNVGILSRFLON	PLMIFHLFCAYGHATNMK	TDYANPFVMVKNWSRNN	764	
QY	806	--SQTMGAVFEDLPKMPFGSTHLL--	TAPFLGALGIYSSLSHFT	EVGAYPRSFSTKTP	861	
Db	765	CWALIECGGS----MPLLVFENGRL	FQGAIFPMKLQLVYAYHG	DFKETTADGRFRSNGS-L	819	
QY	862	INVLPVIGKGSFNNAQRQPAWTVEL	AYQVLYRQEPGIATQLLASK	GIWFGSGSPSSR	921	
Db	820	TSISVPLGIREKL-ALSQDVL	YDFSYSYIPDIFRKDPSC	EAAALVSGDSWLVPAAHVSR	878	
QY	922	HA	923			
Db	879	HA	880			
RESULT 13						
US-10-023-437-23						
; Sequence 23, Application US/10023437						
; Publication No. US20020183272A1						
; GENERAL INFORMATION:						
; APPLICANT: JOHNSTON, STEPHEN A.						
; APPLICANT: STEMKE-HALE, KATHERINE						
; APPLICANT: SYKES, KATHRYN F.						
; APPLICANT: KALTENBOECK, BERNHARD						
; TITLE OF INVENTION: METHODS AND compositions for Vaccination COMPRISING						
; TITLE OF INVENTION: AND/OR POLYPEPTIDE SEQUENCES OF CHLAMYDIA						
; FILE REFERENCE: US/10/023,437						
; CURRENT APPLICATION NUMBER: 2001-12-17						
; PRIOR FILING DATE: 2001-12-17						
; PRIOR APPLICATION NUMBER: 60/225,839						
; PRIOR FILING DATE: 2000-12-15						
; NUMBER OF SEQ ID NOS: 69						
; SOFTWARE: PatentIn ver. 2.1						
; SEQ ID NO 23						
; LENGTH: 839						
; TYPE: PRT						
; ORGANISM: Chlamydia psittaci						
US-10-023-437-23						

Query Match	10.4%;	Score 531;	DB 9;	Length 839;
Best Local Similarity	25.6%;	Pred. No. 8.le-33;		
Matches 232;	Conservative 129;	Mismatches 347;	Indels 198;	Gaps 44;
Qy	167	HDVVGFEMKFSYVRGGAISTAN-----TFVYSENQK--CFLEFMDNI	205	
		:		
Db	3	HPVWFLLISSLFASNLUSFANDAQTALTPSDSYNGNVTSEEFQYKETSSTTTCBGNV	62	
		:		
Qy	206	CIQNTAGKGGAI-----YAGTSTN-SFESNCCDLFFINNACCA-----	242	
		:		
Db	63	CI--SFAGKDSGLKKCSFASDNLTLFLNGNYTLCEDNTTTTASNPGAINVOGQKTLGIS	120	
Qy	243	GGAI FPSICS-----LTG-----NRGNITVFYNNRCF-----KNVETASSEASDGGAIKVTR	289	
		:		
Db	121	GFSLSF--CAYCPPTCTCYGAIOATKNTTLKDNSSLVPHKNCSTV-----EGGAIQCKGS	173	
		:		

QY 870 --VKGSFNNATQRPQAW-----TVLAYOPVLYROEPGIATOLLASKGIWFGSGSPSS 920
 Db 1627 FSVDPAL-----ANREILYNKVSAAVLPVILRNPKATYEVLSKKEGNNVNVLP 1678
 QY 921 RHAMYSKISQOTQPLSWLTHFQYHGYSSSTFCNYLNGEIALRF 965
 Db 1679 RNAARAEVSSQIYLGSYWTLYGTITDASMTLVOMANGGIRFVF 1723

RESULT 15
 US-09-841-132-395
 ; Sequence 395, Application US/09841132
 ; Patent No. US20020061848A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bhatia, Ajay
 ; APPLICANT: Skeiky, Yasir A.W.
 ; APPLICANT: Probst, Peter
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
 ; TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
 ; FILE REFERENCE: 210121.469C8
 ; CURRENT APPLICATION NUMBER: US/09/841,132
 ; CURRENT FILING DATE: 2001-04-23
 ; NUMBER OF SEQ ID NOS: 599
 ; SOFTWARE: FastSeq for Windows Version 3.0/4.0
 ; SEQ ID NO 395
 ; LENGTH: 1723
 ; TYPE: PRT
 ; ORGANISM: Chlamydia pneumoniae
 US-09-841-132-395

Query Match 10.2%; Score 517; DB 10; Length 1723;
 Best Local Similarity 22.8%; Pred. No. 2.9e-31;
 Matches 257; Conservative 164; Mismatches 446; Indels 258; Gaps 50;

QY 15 SGLAREVPSRIFL-----MPNSVDPDKESLSNKSISLTDGTHMLT-----NCYLDNL 61
 Db 683 NGGANYPENIVLTFTYTPNE--PAVQOPVYGEALVTGNTATKSGGGIYTKNAAFSL 741

QY 62 RYILAILQKTPNEGAATIT---DYLSEFDQKEGYFAKNLTPESSGAIG-----YAS 112
 Db 742 SSV--TFQNTSSSENGGALLTQKADKDCSFYITVNTNTATNGGGIAGGKAHFR 800

QY 113 PNSTVEIRDTI--GPVIFENNTCCRPFT--SSNPNAVNKIREGGAIHAQNLIN---- 164
 Db 801 IDNLTQSNQAKGGGVLEDALEKLVITGSVSQNTAT--ESGGIYAKDIQLQALPG 857

QY 165 ----HNDVYVGMKNSFYVGGALSTANTFVSENQSCFLPMONICITQNTAG-----KGG 216
 Db 858 SFTITDNKVTSLTSTNLXGGIYSSGAVTLTNISGFTGITSVINTATSDADIQGG 917

QY 217 AIYAGTSNFSNCDLFFINNACC-----AGGAIFSPICSLTGNRGNTIVEYNNR 266
 Db 918 GIATSLSLNQCNTPIFLSNSAAYKKTSTTKQIAGGAIFSAAVTIENNSQPIIFLUNS 977

QY 267 CFKNVETAS---SEASDGGAI-----KVTR-----LDVT----- 293
 Db 978 AKSEATTAATAGNKGCGGAIAANSVLTNNPEITPKGNYAETGGAIGCIDLINGSPPRK 1037

QY 294 ---GNRGRIFFSNITKNYGAIYAPVTVLDNGPTYFINNIANNKGGAIYIDGTSNSKI 350
 Db 1038 VSIADNGSVLFQDNALNRGGAIGYGETIDISRTGAT--FIGNSKHDGSAIC---CSTALT 1093

QY 351 SADRHAIENENIVNTV-----NANGTSTSANPPRRAITVASSSGEIL----- 395
 Db 1094 LAPNSQLIFENNKVTETATTAKSINNLAGAAYGNNTSDITISLSAENGSIFFKNNLCT 1153

QY 396 -----LGAGSQNLIFYDPLEVSNAQVS---VSFNKEADQGTGSVPFSGA 436
 Db 1154 ATKYCSIAQNVKETAESAGKAISFYDAVNVSTKETAQELKLEKATSTGTILFSG- 1212

QY 437 TVNSADPHQNLQTKTPAPITLNGFLICIEDHAQLTVNRFOT--GGVYSLGNGAVLSCYK 495

Db 1213 -----ELHEN--KSYIPQKVTFAHGNLILCKNAELSVVSTQSPGTTITMGPGSVLSNHS 1265
 QY 496 NGAGNSASNIATLKHIGLNLSSL--KSGAEI---PLLWVEPTNNSNNTATATATFSL 550
 Db 1266 KEAG-----GIAINNVIIDFSEIVPTKDNATVAPTLKLVSRTNADSKDKIDITGVTL 1319
 QY 551 SDVKLSLIDDDYGNSPY--ESTDLTHALSSQPMLSISEASDNQLRSDDMDFSGLANVPHYGWQ 609
 Db 1320 LDPNGL---YQNSYLGEDRDIT-----LFNIDNSASGAVTATNTVLOGNLGAKGYL 1369
 QY 610 GLMTGWAKTQDPEPASAITDPQKANRHRHRTLLTW-----LPAGYVSPKXHSPLIA 664
 Db 1370 GTW-----NLDPNSSGS-----KIILKWTEDKYLWPIPRDNH---FYI 1406
 QY 665 NTLWG--NMLLATES-----LKNSAELTPSDHPFWGITGGGLGMMVYQDPRENHPGFHM 716
 Db 1407 NSIWAQNSLTVTKQIGILGNMLNNAFEDPAFNNFW---ASAIGSFURKEVSRNSDSFTY 1463
 QY 717 RSSGYSAGMIAGOTHTFSL--KFSQTYTKLERYAKNNVSSK--NYSCQ-----GEMLF- 766
 Db 1464 HGRGYTAADVAKPRQEFILGAATFQVFGHAESYHLDNYKHKGSGHSTQASLYAGNIFYF 1523
 QY 767 -SLOGEFLTKLVGLYSYGDHCHHFFY--TQGENLTSQGTFRSQTMGAVFDLPM---- 819
 Db 1524 PAIRSRPILFQGVATYGYMQRDITTTTYPYSIEEKNMANWDSI-----AWLFDLRFSDVL 1576
 QY 820 ---KPGSTHILTAFLGALGIYSSLSH-----FTEVGAYPRSFSTKTPLINVLVPIG 869
 Db 1577 KEPQPHSTAR-----LTFYEAETRIROEKFTELDYDPRFSA--CSYGNLAIPGT 1626
 QY 870 --VKGSFNNATQRPQAW-----TVLAYOPVLYROEPGIATOLLASKGIWFGSGSPSS 920
 Db 1627 FSVDPAL-----ANREILYNKVSAAVLPVILRNPKATYEVLSKKEGNNVNVLP 1678
 QY 921 RHAMYSKISQOTQPLSWLTHFQYHGYSSSTFCNYLNGEIALRF 965
 Db 1679 RNAARAEVSSQIYLGSYWTLYGTITDASMTLVOMANGGIRFVF 1723

Search completed: February 4, 2003, 21:08:42
 Job time : 81 secs

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OM protein - protein search, using sw model

Run on: February 4, 2003, 20:53:42 : Search time 94 Seconds
(without alignments)
2115.271 Million cell updates/sec

Title: US-09-677-752-2
Perfect score: 5086
Sequence: 1 MKKAFFFLIGNSLGLARE.....GFYSSSTFCNYLNGEIALRF 965

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL.21.*
1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phage.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*
15: sp_virus.*
16: sp_bacteriap.*
17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	636	12.5	926	2 P71135	P71135 chlamydophi
2	544.5	10.7	847	2 P71132	P71132 chlamydophi
3	531	10.4	839	2 P77792	P77792 chlamydia p
4	530.5	10.4	772	16 Q9RB71	Q9RB71 chlamydia p
5	530.5	10.4	846	2 P71133	P71133 chlamydophi
6	512	10.1	392	16 Q9Z881	Q9Z881 chlamydia p
7	477	9.4	700	2 Q8VU50	Q8VU50 chlamydia p
8	422	8.3	347	16 Q9RB61	Q9RB61 chlamydia p
9	387	7.6	1530	2 Q93QE8	Q93QE8 chlamydia t
10	349	6.9	602	2 Q8VU49	Q8VU49 chlamydia p
11	346.5	6.8	581	2 Q8VU48	Q8VU48 chlamydia p
12	344.5	6.8	601	2 Q8VL57	Q8VL57 chlamydia p
13	321	6.3	494	16 Q9RB68	Q9RB68 chlamydia p
14	297	5.8	427	16 Q9RB70	Q9RB70 chlamydia p
15	275.5	5.4	445	16 Q9RB67	Q9RB67 chlamydia p
16	253.5	5.0	359	16 Q9JSK6	Q9JSK6 chlamydia p

17	249	4.9	649	2 P71134	P71134 chlamydophi
18	234.5	4.6	1250	16 Q8XE28	Q8XE28 escherichia
19	224	4.4	989	2 Q9XD84	Q9XD84 escherichia
20	213	4.2	2902	16 Q9ZME6	Q9ZME6 helicobacte
21	206	4.1	1364	2 Q8VSL2	Q8VSL2 shigella fl
22	205.5	4.0	820	12 Q89364	Q89364 paramecium
23	204	4.0	1604	2 Q9KK99	Q9KK99 rickettsia
24	203	4.0	1654	2 Q93QW9	Q93QW9 rickettsia
25	202	4.0	2399	16 Q9ZKS9	Q9ZKS9 helicobacte
26	201.5	4.0	1487	16 Q8YK40	Q8YK40 anabaena sp
27	201.5	4.0	1881	16 Q8RGK2	Q8RGK2 fusobacteri
28	201	4.0	1029	2 Q52708	Q52708 rickettsia
29	200.5	3.9	1369	12 Q89349	Q89349 paramecium
30	200.5	3.9	1620	2 Q9KKB5	Q9KKB5 rickettsia
31	200	3.9	2893	16 Q25063	Q25063 helicobacte
32	199.5	3.9	1102	2 Q52298	Q52298 shigella fl
33	199.5	3.9	1102	2 Q99Q93	Q99Q93 shigella fl
34	198.5	3.9	1335	12 Q89353	Q89353 paramecium
35	197.5	3.9	1304	2 Q9XC46	Q9XC46 rickettsia
36	196.5	3.9	1649	16 Q9CFA2	Q9CFA2 lactococcus
37	195	3.8	1364	2 Q99QC6	Q99QC6 shigella fl
38	195	3.8	1618	2 Q9KKB4	Q9KKB4 rickettsia
39	195	3.8	1619	2 Q9KKB7	Q9KKB7 rickettsia
40	194	3.8	1603	2 Q9KKA6	Q9KKA6 rickettsia
41	194	3.8	1643	2 Q9F0P7	Q9F0P7 rickettsia
42	193	3.8	1616	2 Q9KKA5	Q9KKA5 rickettsia
43	192.5	3.8	2529	16 Q25579	Q25579 helicobacte
44	192	3.8	1070	16 Q8ZA36	Q8ZA36 yersinia pe
45	192	3.8	1072	2 Q9F288	Q9F288 yersinia pe

ALIGNMENTS

RESULT 1

ID	P71135	PRELIMINARY;	PRT;	926 AA.
AC	P71135;			
DT	01-FEB-1997 (TREMBLrel. 02, Created)			
DT	01-FEB-1997 (TREMBLrel. 02, Last sequence update)			
DT	01-JUN-2002 (TREMBLrel. 21, Last annotation update)			
DE	Putative 98 kDa outer membrane protein.			
OS	Chlamydophila abortus.			
OC	Bacteria; Chlamydiales; Chlamydiaceae; Chlamydophila.			
OX	NCBI_TaxID=83555;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-OVINE ABORTION S26/3;			
RA	Longbottom D., Russell M., Dunbar S.M., Jones G.E., Herring A.J.;			
RT	"98kDa protein genes from ovine abortion strain S26/3 Chlamydia			
RT	psittaci."			
RL	Submitted (SEP-1996) to the EMBL/GenBank/DBSJ databases.			
DR	EMBL; U724599; AAB18188.1; -			
DR	InterPro; IPR003368; Chlamydia_PMP.			
DR	InterPro; IPR003357; OMP.			
DR	Pfam; PF02415; DUF145; 2.			
DR	Pfam; PF02385; OMP; 1.			
SQ	SEQUENCE 926 AA; 98439 MW; 3E755E52F594750F CRC64;			

Query Match	12.5%;	Score 636;	DB 2;	Length 926;
Best Local Similarity	24.0%;	Pred. No. 5.4e-29;		
Matches 241;	Conservative 157;	Mismatches 365;	Indels 240;	Gaps 41;
QY	41	SNKISUTGTHNL--TNCYLDNRLYLAILQKTPNEGA-----AVITDY--L 84		
Db	82	ADNLTFKGNHSLITNA-----NAGANPAGINVNTADKILTLTDFSKL 125		
QY	85	SFEDTQKEIGYFAKNLTPESGGAIGYASPNSTPVEIRDTIGPVIFENWTCRPFSSNPN 144		
Db	126	SPKECFSSLVNVTGKG-AMKSGGALNLANAS-----ILFDQN-----YSAEN-- 166		
QY	145	AAVANKIREGGATHAONLYNHNDHVVGFMKNFSYVRGGAISTANTFVWSENGSCFLFMDN 204		

Db	167	-----GGAIKCAKSLTGGSSKEISFTTNTAKKGAIAATGIAHLSDNQGTIRFSGN	218
Qy	205	ICITNTAGKGGAIIAGTINSFESNNCDLFIINNACC-----AGGAIFSPICSLTNGRGN	259
Db	219	TAVNS-----CGAVYSEASMTIAGNN-HVAFSNNAVSGSDGCGGAIH---CSKTGSAPT	269
Qy	260	IVFYNNRCFKNVETASSEADSGGAIKVTTRLDVTGNRGIFFSDNTIKYGGAIYAPVVT	319
Db	270	LTIRDNV-----LIPENTSSAKGGAITYDKLI	298
Qy	320	LVDNGPYFIINN-----IANNKGAIYIDGTSNSKISADRAHAIFENENIVTNVANGTSTS	376
Db	299	LTSGGPTAFINNKVTHPATPKGGAGIAANGECSLTAHEGDITFDNKLMTAQDNAT-----	353
Qy	377	ANPPRRNAITVASSSGRILLGAGSSONLIFYDPIEV-SNAGVSVSFENK-EADQT--GSVY	432
Db	354	---TKRNAINTEGCKFVNLRASGKTSIFYDPIETVEGNAADLLTLNKAEGDKTYNGRII	410
Qy	433	FSGATVNS-----ADFHORNLOTKTAPAPLTLSSNGFLCIEDHAOLTYNNRTQTGGVVS	487
Db	411	FSGEKLTTEEQAADVAD---NLKTTFTQPTILAAAGELVLRSGVEAKTVVQTAGSLILMD	466
Qy	488	GAVLSCYKNGAGNSASNASITLKHIGLUNSSI-----LKSGAEIPLW---VBP	533
Db	467	A-----GTLKSAKTEDATLNALNPMTLDGKGFVAVDAVAAKNTVLSGAIGVIDP	518
Qy	534	TNN--SNNYTADTAATSLSDVKLSLIDDYGNSPYESTDL-THALSSQPMLSISEASDNO	590
Db	519	TGKYEYENHKNDTLUA---LGGIQLS-----GKGSVTTINVPVSHV-----	555
Qy	591	LRSDMDDFSGINPHYGWOGIWTGWAKTODPEPASSATITDPQKANRPHRTILLTLWLP	650
Db	556	-----GVAETHYGYQGNWSVSWKDNNSDKPT-----QTAIFTWNT	592
Qy	651	GYVPSPKHRSPLIANTLWGNMLLATSLSKNSABELTSPD--HPFWGITGGGLGMVYQDPR	708
Db	593	GYVNPERRAPLVLNLSWGS-FIDRLSIQDVLERSVDSILETRGLWWSGIGNFTFKDRN	651
Qy	709	ENHPGCFHMRSSGYSAGMIAGQTH--TFSLKFSQTYTKLNERAKKNVSS-----	755
Db	652	AENRKRFRHISGCVYVLGATTNTSREDSLSVAFQCLFAKDKDYLVSKNAAVYAGSVYQHV	711
Qy	756	-----KNYSCQEMFLSLOEGFLLTKLVGLYSYGDHNCHEFTYGTENLTSGQT	803
Db	712	SKFDDLTRLFNGPNWTCSSG---FSKEIPIFLDAQI-TYCHTANNMTITSYDIPEV--KGS	765
Qy	804	FRSOTMGGAFFDLPMPKPGFSHTILT-APPLGALGIYSSLSHFTEYGAYPRSFSTKPLI	862
Db	766	WGNDLTGLTSLTSPVIPVFSSSIFDSVAPFAKLQVVIYAHQDDFKEPTTEGRVFES-SDLL	824
Qy	863	NVLPIGVKGSFNPNAQPOAWTVELAYQPVLYRQEPGIATOLLASKGTWFGSGSPSRH	922
Db	825	NVSPIGIKFEKLSYGER-SAYDOLTLMYIPDVYRHNPSGMTGLAINDSWLTATNARQ	883
Qy	923	AMSKISQOQTOPLSWTLFHFQYHGEYSSSTECNY-----LNGEIA	962
Db	884	AFIVRAGNHIALTSGVEMFSQF-GFELRSSRNYNDLGAKVA	925
RESULT 2			
Db	P71132	PRELIMINARY; PRT; 847 AA.	
AC	P71132		
DT	01-FEB-1997	(Tremblrel. 02, Created)	
DT	01-FEB-1997	(Tremblrel. 02, Last sequence update)	
DT	01-JUN-2002	(Tremblrel. 21, Last annotation update)	
DE	POWP91A.		
OC	Chlamydomophila abortus		
OC	Bacteria; Chlamydiales; Chlamydiaceae; Chlamydomophila.		
NCBI	NCBI_taxid=83555;		
RC	SEQUENCE FROM N.A.		
RC	STRAIN=S26/3.		

QY	458	LSNGFLCIEDHAOLQTVNRFTQ--TGGVVSLGNGAVLSCYKNGAGNSASNIITLKHGLNL	516
QY	459	LSAGSLVLKDGVSATKQVQTQAGSTVMDLGTTLQTPSSG-----GETITETNDINI	398
Db	345	LSAGSLVLKDGVSATKQVQTQAGSTVMDLGTTLQTPSSG-----GETITETNDINI	398
QY	517	SSILKSGAIEPLLVVEPTNNSNYTADTAATFSLDSVKLSLIDDDYGNPSYESTDLTHALS	576
Db	399	ASLGGGGG-----TSPAKLATN-TASQALITN-----AVNLVDADGNA-YEDPILA---T	443
QY	577	SOPMLSIASEADNQLRSDDDMFSGLNVP--HYGQGLWTGWAKTQDPEPASSATITDPQ	634
Db	444	SKPPTAIVATNASTVTQPTDNLNTNVPPTHYGYQGNTVTW---DTETAT-----	491
QY	635	KANRFHRTLLLTWLPAGYVSPKHRSPLIANTLWG--NMLLATESLKN-SAEITPSDHPF	691
Db	492	-----KTATLTWEQTGYSPNERQGLVPNTLWGAFSDLRAIQNLMDISVNGADYHRGF	545
QY	692	WGITGGGLGMWYQDPRNHPGFHMRSSGYSAGMIA--GQHTFTSLKFSQTYTKLNERYA	749
Db	546	W---VSLGANFLHKSGSDTKRKRPHNSAGVALGVYAKTSPDDIDFSAFCOLFCK-----	597
QY	750	KNNVSKNYSCQGEMLFSLQEGFLTLKVLGYLSYGDH-----NCHH	790
Db	598	KDVLVSKNNA-----NIYAGSLYQHISYWSAWQNLQNTIGAEAPLVNLQAITYCHA	650
QY	791	FYTOGENLTS-----OQTPRSQTMGCAVFPDLPMKPPFGSTHI--LTAPFLGALG	837
Db	651	SNDMKTNMTTYYAPKTTYAEIKDGMGNCFCVELGATVPIDQTESLLFDMYSPFLKQFL	710
QY	838	IYSSLSHFTVEGAYPRFSFTKTLPLNLVPIGVKGSFMMNATQPAWTVLAYQPVLRYQ	897
Db	711	VHTHQDDFKENNSDQGRYFESSNLTNLSPGKFERF-ANNDTASYHVTAAYSPDIVRS	769
QY	898	EPGIATOLLAS--KGIWFGSGSSRRHMSYKISQQTQPLSWTLH-----FOYHGFP--	948
Db	770	NPQCTTSLLYSPDSAVVWTKANLARSF-----MLQAGNYLSLSHNIEIFSQGFELR	823
QY	949	-SSSTF	953
Db	824	GSSRTY	829
RESULT 4			
Q9RB71	ID	Q9RB71	PRELIMINARY; PRT; 772 AA.
AC	Q9RB71		
DT	01-MAY-2000	(TEMBLrel. 13, Created)	
DT	01-OCT-2000	(TEMBLrel. 15, Last sequence update)	
DT	01-JUN-2002	(TEMBLrel. 21, Last annotation update)	
DE	Pmp. 3.		
GN	PMP_3.2.		
OS	Chlamydia pneumoniae (Chlamydophila pneumoniae).		
OC	Bacteria; Chlamydiales; Chlamydiaceae; Chlamydophila.		
OX	NCBI_TaxID=83558;		
RP	[1]		
RN	SEQUENCE FROM N.A.		
RC	STRAIN=J138;		
RC	MEDLINE=20330349; PubMed=10871362;		
RA	Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K.,		
RA	Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.;		
RT	"Comparison of whole genome sequences of Chlamydia pneumoniae J138		
RT	from Japan and CW1029 from USA.";		
RL	Nucleic Acids Res. 28:2311-2314(2000).		
DR	EMBL: AP002545; BAA98226.1; -		
DR	InterPro: IPR003368; Chlamydia_pmp.		
DR	InterPro: IPR003357; OMP.		
DR	Pfam: PF02415; DUF145; 1.		
DR	Pfam: PF02385; OMP; 1.		
SQL	SEQUENCE	772 AA; 82931 MW; 484FC56D635801EB CRC64;	
Query Match			
Best Local Similarity		10.4%; Score 530.5; DB 16; Length 772;	
Matches 221; Conservative 124; Mismatches 343; Indels 167; Gaps		25.8%; Pred. No. 6.3e-23;	

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QY 172 FMKNFSYVRGGAISTANTFVVSQSCFLFMDNICIQTNTAGKGAIYAGTNSFSFNNC 231
Db 172 FMKNFSYVRGGAISTANTFVVSQSCFLFMDNICIQTNTAGKGAIYAGTNSFSFNNC 231
QY 3 FSKNFSTDNGGAI-TAKTILSLTGTWALSFSN-----TSSKGGAIQTSALTITNGQ 56
Db 3 FSKNFSTDNGGAI-TAKTILSLTGTWALSFSN-----TSSKGGAIQTSALTITNGQ 56
QY 232 DLEFFINNACC-AGGAIFFSPICSLTGNRGNIVFVNNRCFKNVETASSEAS---DGGAI--- 284
Db 232 DLEFFINNACC-AGGAIFFSPICSLTGNRGNIVFVNNRCFKNVETASSEAS---DGGAI--- 284
QY 57 EVSFSNTSDSGAAIATEASVTISNAKVSFIDNK---VTGASSSTTGDMSGGAICAY 112
Db 57 EVSFSNTSDSGAAIATEASVTISNAKVSFIDNK---VTGASSSTTGDMSGGAICAY 112
QY 285 --KVTRLDVTGNRGRIFFSDNITTKYGGAIYAPVVTVLDVNGPTYFINNIANN---KGG 338
Db 285 --KVTRLDVTGNRGRIFFSDNITTKYGGAIYAPVVTVLDVNGPTYFINNIANN---KGG 338
QY 113 KYSTDTKVTLTGQ--MLFSNNTSTAGGAIYVKLELASGGTLTFSRVNGTGAPKGG 171
Db 113 KYSTDTKVTLTGQ--MLFSNNTSTAGGAIYVKLELASGGTLTFSRVNGTGAPKGG 171
QY 339 AIYIDGTSKISADRAHAIIFENIVNTVNTANGTSTANPPRRNAITVASSSGEILLGA 398
Db 339 AIYIDGTSKISADRAHAIIFENIVNTVNTANGTSTANPPRRNAITVASSSGEILLGA 398
QY 172 ATAIEDSGELSDSGDIVLGNVTYSIT--PGTN-----RSSIDLGTSKWTALRS 222
Db 172 ATAIEDSGELSDSGDIVLGNVTYSIT--PGTN-----RSSIDLGTSKWTALRS 222
QY 399 GSSONLIFDPTIEVSNAQVSFVNK-----EADQ-----TGSVVSFGATVNSAD-FHORNLO 449
Db 399 GSSONLIFDPTIEVSNAQVSFVNK-----EADQ-----TGSVVSFGATVNSAD-FHORNLO 449
QY 223 AAGRAIYFDYDPTTGGSTTVTDVLYKNETPADSALQYTGNIIFTGEKLSETEAAADSKNLT 282
Db 223 AAGRAIYFDYDPTTGGSTTVTDVLYKNETPADSALQYTGNIIFTGEKLSETEAAADSKNLT 282
QY 450 TKTPTPLTSLNGFLCIEDHAQTLVNRFTOTGGVVSGLNGAVLSCYKNGAGNASNA-SIT 508
Db 450 TKTPTPLTSLNGFLCIEDHAQTLVNRFTOTGGVVSGLNGAVLSCYKNGAGNASNA-SIT 508
QY 283 SKLLQPVTLSSGTLKHKGVTLTQTAFTQAD-----SRLEMDVGTTLTLEPADTST 332
Db 283 SKLLQPVTLSSGTLKHKGVTLTQTAFTQAD-----SRLEMDVGTTLTLEPADTST 332
QY 509 LKHIGLNLSSILKSGAEIPLLVWEPTNNSNNTADTAATFSLSDVLSLIDIDYNSPYES 568
Db 509 LKHIGLNLSSILKSGAEIPLLVWEPTNNSNNTADTAATFSLSDVLSLIDIDYNSPYES 568
QY 333 INNLVINISSI--DGAK--KAKIETKATSKNLT--LSGTLTLLDPTGTYEHNLSRNPQS 386
Db 333 INNLVINISSI--DGAK--KAKIETKATSKNLT--LSGTLTLLDPTGTYEHNLSRNPQS 386
QY 569 TDLTHALSOPMLISSEASDNQLRSDMDPSGLNVP-----HYGQGLW---TWGWAQT 619
Db 569 TDLTHALSOPMLISSEASDNQLRSDMDPSGLNVP-----HYGQGLW---TWGWAQT 619
QY 387 YDILELKASGTVTSTAVTPD-----PIMGEKPHYGYGTGWGPIVWG--- 427
Db 387 YDILELKASGTVTSTAVTPD-----PIMGEKPHYGYGTGWGPIVWG--- 427
QY 620 QDPEPASSATITDPOKANRFRHTLLTLWLPAGVVPSPKHSPLIANTLWGNMLLATESL- 678
Db 620 QDPEPASSATITDPOKANRFRHTLLTLWLPAGVVPSPKHSPLIANTLWGNMLLATESL- 678
QY 428 -----TGASTAT-----FNWTKGTIPNPERIGSLVNPNSL-NAFIDISSLH 469
Db 428 -----TGASTAT-----FNWTKGTIPNPERIGSLVNPNSL-NAFIDISSLH 469
QY 679 ---KNSAELTPDHPFWGTGGGLGMVYQDPRENNHGFPHMRSSSGYSAGIAGQTHFSL 735
Db 679 ---KNSAELTPDHPFWGTGGGLGMVYQDPRENNHGFPHMRSSSGYSAGIAGQTHFSL 735
QY 470 YLMETANEGLQDRAFW---CAGLSNFFHKDKTKTRRGFRHLSGGY---VIGNLHTCSD 523
Db 470 YLMETANEGLQDRAFW---CAGLSNFFHKDKTKTRRGFRHLSGGY---VIGNLHTCSD 523
QY 736 K-----FSQTYTKLNEY-AKNN---VSSKNYSCOGEMFLFSL-----QEGFLTKLVG 779
Db 736 K-----FSQTYTKLNEY-AKNN---VSSKNYSCOGEMFLFSL-----QEGFLTKLVG 779
QY 524 KILSAFAOLFGRDRDYFAKNQGTGYGTLXYQHNETYISLPCRLPCSLSVPTPIPV 583
Db 524 KILSAFAOLFGRDRDYFAKNQGTGYGTLXYQHNETYISLPCRLPCSLSVPTPIPV 583
QY 780 LYSYGDHCHHFYTOGENLTSGTFRSQDMGAVFEDLPKPFSGTHILT----- 829
Db 780 LYSYGDHCHHFYTOGENLTSGTFRSQDMGAVFEDLPKPFSGTHILT----- 829
QY 584 LFS---GNLSYTHDNDLTKYTY--PTVKSGWGNDSFALFEGGRAPICLDESALFEQY 638
Db 584 LFS---GNLSYTHDNDLTKYTY--PTVKSGWGNDSFALFEGGRAPICLDESALFEQY 638
QY 830 APFLGALGYISLSHFTVEGAYPRSFSTKPLINLVPIGVK-----GSPMNATQRPAWT 885
Db 830 APFLGALGYISLSHFTVEGAYPRSFSTKPLINLVPIGVK-----GSPMNATQRPAWT 885
QY 639 MPFMKLQFYAHQEGFKEQGTAREFGS-SRLVNLALPIGIRFKESDCQDAT-----YN 692
Db 639 MPFMKLQFYAHQEGFKEQGTAREFGS-SRLVNLALPIGIRFKESDCQDAT-----YN 692
QY 886 VELAYOPVLYROEPPGIATOLLASKGIWFGSGSPSRHMSYKISQOTQPLSLWTLHFQYH 945
Db 886 VELAYOPVLYROEPPGIATOLLASKGIWFGSGSPSRHMSYKISQOTQPLSLWTLHFQYH 945
QY 693 LTLGTVTLVRSNPDCPTTLRLRISGDSWKTGFTNLARQALVLRAGN-----HFCFN 742
Db 693 LTLGTVTLVRSNPDCPTTLRLRISGDSWKTGFTNLARQALVLRAGN-----HFCFN 742
QY 946 -GFYSSTFCNYLNG 959
Db 946 -GFYSSTFCNYLNG 959
QY 743 SNFAFSQSFELRG 757
Db 743 SNFAFSQSFELRG 757
RESULT 5
P71133
ID P71133 PRELIMINARY; PRT; 846 AA.
AC P71133;
DT 01-FEB-1997 (TReMBLrel. 02, Created)
DT 01-FEB-1997 (TReMBLrel. 02, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE POMP91B precursor.
OS Chlamydia abortus.
OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxID=83555;
RN [1]
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RP SEQUENCE FROM N.A.
RC STRAIN=S26/3;
RX MEDLINE=96406378; PubMed=8810511;
RA Longbottom D., Russell M., Jones G.E., Lainson F.A., Herring A.J.;
RT "Identification of a multigene family coding for the 90 kDa proteins
of the ovine abortion subtype of Chlamydia psittaci.";
RL FEMS Microbiol. Lett. 142:277-281(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=S26/3;
RX MEDLINE=98187897; PubMed=9529048;
RA Longbottom D., Russell M., Dunbar S.M., Jones G.E., Herring A.J.;
RT "Molecular cloning and characterization of the genes coding for the
highly immunogenic cluster of 90-kilodalton envelope proteins from the
Chlamydia psittaci subtype that causes abortion in sheep.";
RL Infect. Immun. 66:1317-1324(1998).
DR EMBL; U65943; AAC15923.1; -.
DR InterPro; IPR003368; Chlamydia_PMP.
DR InterPro; IPR003357; OMP.
DR Pfam; PF02415; DUF145; 1.
DR Pfam; PF02385; OMP; 1.
KW Signal.
FT SIGNAL.
FT CHAIN.
SQ SEQUENCE 846 AA; 90834 MW; 4CDC31DC03C2964E CRC64;
Query Match 10.4%; Score 530.5; DB 2; Length 846;
Best Local Similarity 24.2%; Pred. No. 7.1e-23;
Matches 239; Conservative 141; Mismatches 361; Indels 245; Gaps 47;
QY 1 MKKAPFFFLIGNSLGLAREVPSRIFLMPNSV--PDPTKESLSNKISLTGDTNHTNLCYL 58
Db 1 MKHPYVWFLISSL-----LASNSLSFAQVTNETLTSSDSYNG---NVT---- 41
QY 59 DNLRYLAILQKTPNEGAAVTIDYLSFPDQKEGIYFAKNITPESGGAIYASPNSPV 118
Db 59 DNLRYLAILQKTPNEGAAVTIDYLSFPDQKEGIYFAKNITPESGGAIYASPNSPV 118
QY 42 -----SDEFEVKETTSGAIY-----TCEGNVCISYAGKDSPL- 73
Db 42 -----SDEFEVKETTSGAIY-----TCEGNVCISYAGKDSPL- 73
QY 119 EIRDTIGVIFENNCCRPFTSSNPNAAVNKIREGAIHAQNLVYHNHHDVGVFKNFYS 178
Db 119 EIRDTIGVIFENNCCRPFTSSNPNAAVNKIREGAIHAQNLVYHNHHDVGVFKNFYS 178
QY 74 -----NKSCFSETT-----ENUSF 87
Db 74 -----NKSCFSETT-----ENUSF 87
QY 179 VRGGAISTANTFVVSQSCFLFMDNICIQTNTAGKGAIYAGTNSFSFNNCDLFFINN 238
Db 179 VRGGAISTANTFVVSQSCFLFMDNICIQTNTAGKGAIYAGTNSFSFNNCDLFFINN 238
QY 88 ICGN-----YTLCF--DN--ITQSSHPGAIYSVSGTNKTLDISGSLFSCAY 130
Db 88 ICGN-----YTLCF--DN--ITQSSHPGAIYSVSGTNKTLDISGSLFSCAY 130
QY 239 ACCAG-----GAIFFSPICSLTGNRGNIVFVNNRCFKNVETASSEADGGAIKY-----TTR 289
Db 239 ACCAG-----GAIFFSPICSLTGNRGNIVFVNNRCFKNVETASSEADGGAIKY-----TTR 289
QY 131 CCPPTGTGYATQTKGTTTKDNSSLVFH-----KNCSTA-----EGGAIQCSSTAE 180
Db 131 CCPPTGTGYATQTKGTTTKDNSSLVFH-----KNCSTA-----EGGAIQCSSTAE 180
QY 290 LDVTGNRGRIFFSDNITTKYGGAIYAPVVTVLDVNGPTYFINN-IANN---KGAIVY-DG 344
Db 290 LDVTGNRGRIFFSDNITTKYGGAIYAPVVTVLDVNGPTYFINN-IANN---KGAIVY-DG 344
QY 181 LXLENNK-NLVESENSSKEKGAIYADKLITVSGGPTLFSNNSVSHNSPKGCAICIKDS 239
Db 181 LXLENNK-NLVESENSSKEKGAIYADKLITVSGGPTLFSNNSVSHNSPKGCAICIKDS 239
QY 345 TSNKISADRAHAIIFENIVNTVNTANGTSTANPPRRNAITVASSSGEILLGAGSSQNL 404
Db 345 TSNKISADRAHAIIFENIVNTVNTANGTSTANPPRRNAITVASSSGEILLGAGSSQNL 404
QY 240 DGECSLTANLGDITFDGN---KIITNGSGPTVT---RNSIDLGGSGKFTKLNAKEGFI 293
Db 240 DGECSLTANLGDITFDGN---KIITNGSGPTVT---RNSIDLGGSGKFTKLNAKEGFI 293
QY 405 IFYDPIEVSNAQVSFVNK-EAD--QTGSVVSFGATVNSAD-FHORNLOKTPAPLTLN 460
Db 405 IFYDPIEVSNAQVSFVNK-EAD--QTGSVVSFGATVNSAD-FHORNLOKTPAPLTLN 460
QY 294 FFYDPIANTGGSTELNKTESDITYTKIVFSGEKLDEEKTVPANLKSYPKPKLTKGA 353
Db 294 FFYDPIANTGGSTELNKTESDITYTKIVFSGEKLDEEKTVPANLKSYPKPKLTKGA 353
QY 461 GFLCIEDHAQTLVNRFTOT--GGVVSGLNGAVLSCYKNGAGNASNASITLKHIGLNLSSI 519
Db 461 GFLCIEDHAQTLVNRFTOT--GGVVSGLNGAVLSCYKNGAGNASNASITLKHIGLNLSSI 519
QY 354 GSLVLKDGVTLEAKKITQTKGSTVVMDLGTLTQT-----PSSSGETTLTNDLINIASL 407
Db 354 GSLVLKDGVTLEAKKITQTKGSTVVMDLGTLTQT-----PSSSGETTLTNDLINIASL 407
QY 520 LKSGAEIPLLVWEPTNNSNNTADTAATFSLSDVLSLIDIDYNSPYESTDLTHALSQOP 579
Db 520 LKSGAEIPLLVWEPTNNSNNTADTAATFSLSDVLSLIDIDYNSPYESTDLTHALSQOP 579
QY 408 GGGGTAPA-----KLATNTASQAISIAAVNLVNTDSNT-YE-----DP 445
Db 408 GGGGTAPA-----KLATNTASQAISIAAVNLVNTDSNT-YE-----DP 445
QY 580 MLSISEA-----SDNQLRSDMDPSGLNVP-HYGQGLTWGWAQTQDPEPASSATI 630
Db 580 MLSISEA-----SDNQLRSDMDPSGLNVP-HYGQGLTWGWAQTQDPEPASSATI 630
QY 446 ILSAKSFSAITATTSSSTVTPPETNLKNYTPPTHYGQGNWTVTW-----KQSSAQ- 498
Db 446 ILSAKSFSAITATTSSSTVTPPETNLKNYTPPTHYGQGNWTVTW-----KQSSAQ- 498
```

QY 631 TDPOKANRFRHRTLLTLPAGYVPSKPHRSPRIANTLWGNMLLATESIKNSAELTPS--- 687
 Db 499 -----EKATLTWFEQTGYSPNPERVGSVLTWNG-AFSDTRAIQNLMDISVNGAD 548
 QY 688 -DHFWGITGGGLGMVYQDPREHNPQFHRKSSGYSGMIAQOT---HTFSLKFSQYTK 743
 Db 549 YSRGFV---VSSLANFLNKSGSDTKRFRHHSAGYALGVYA-QPPSDVCSAAPCQLFGK 604
 QY 744 LNERAKNNYSKNSYCOGEMLF-----LQ-----EGFLLTKLVGLYSYGDHN 787
 Db 605 DKDIFVSKN-SSIIYA--GSIIYOHISYWNWNTLQNTLGAEPVLNLAQLTYCHASN 661
 QY 788 CH-----HFYTOGENLTS---QGTFRSOTMGAVFDFLPMKPFSGTHILTAFLGALGIYS 840
 Db 662 MKTNWNTYTP-KNVTFSEIKDGNWDCFGVEFGAKAPIETASLLDFMYSFPVKQLQVHA 720
 QY 841 SLHSFTVEGAVPRFSFTKTLINVLVPIGVK-GSFMNATORPQAWTVELAYQPVLYROEP 899
 Db 721 HODDFKENNSDOGRYFESNLTLSMPIGVKLEKFSH--KDTASYNLTAYAPDIVRSNP 778
 QY 900 GIATQLLAS--KGIWFGSGSPSRHA 923
 Db 779 DCTASLLVSPTSVAVWTKANNLARHA 804

RESULT 6
 Q92881 ID Q92881 PRELIMINARY; PRT; 392 AA.
 AC Q92881;
 DT 01-MAY-1999 (TrEMBLrel. 10, Created)
 DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
 DE Putative polymorphic outer membrane protein.
 GN PMP_17.3 OR CPN0470.
 OS Chlamydia pneumoniae (Chlamydia pneumoniae).
 OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
 OX NCBI_TaxID=83558;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CWL029;
 RX MEDLINE=99206066; PubMed=10192388;
 RA Kalman S., Mitchell W., Marathe R., Lammel C., Pan J., Hyman R.W.,
 RA Olinger L., Grimwood J., Davis R.W., Stephens R.S.;
 RT "Comparative genomes of Chlamydia pneumoniae and C. trachomatis";
 RL Nat. Genet. 21:385-389(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=J138;
 RX MEDLINE=20330349; PubMed=10871362;
 RA Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K.,
 RA Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.;
 RT "Comparison of whole genome sequences of Chlamydia pneumoniae J138
 from Japan and Cwl029 from USA";
 RL Nucleic Acids Res. 28:2311-2314(2000).
 DR EMBL: AE001631; AAD18611.1;
 DR EMBL: AP002546; BRA98676.1;
 DR InterPro: IPR003357; OMP.
 DR Pfam: PF02385; OMP; 1.
 KW Complete proteome.
 SQ SEQUENCE 392 AA; 44365 MW; 53F20CCA2000AE49 CRC64;
 Query Match 10.1%; Score 512; DB 16; Length 392;
 Best Local Similarity 32.1%; Pred. No. 3e-22;
 Matches 128; Conservative 68; Mismatches 165; Indels 38; Gaps 10;
 QY 579 PMLISASDNLRSDDMDFSGLNV-PHYGWLGTWGWAKTQDPEASSATITDPOKAN 637
 Db 10 PLVLLDVTAKKIDTSLNLIYVAMNLDHYGIQGSYPMWET-----TTTTSSTVPEQTN 64
 QY 638 RFRHRTLLTLPAGYVPSKPHRSPRIANTLW-----GNMLLATESLKN---SABLTP 686
 Db 65 TNHRLVVDVTPVGYRPNRPHGEFIANTLWQSNALLGIRILPPONLKEHDEASLQ- 123

QY 687 SDHPFWGITGGGLGMVYQDPREHNPQFHRKSSGYSGMIA--GQHTFSLKFSQYTKL 744
 Db 124 -----GLLLINQHNRGRKGRNHTTCYAATTSKAPARHSFSLGFAQMFST 172
 QY 745 NERYAKNNYSKNSYCOGEMLFSLQEGFLLTKLVGLYSYGDHN--CHHFTYTOGENLTSQ 802
 Db 173 RERQSPSTSHNYFAGLRFDLSLLFRDIFSTGLSLGYSGDHHMLCH--YTEILKGSKA 230
 QY 803 TFSQTMGGAVFDFLPMKPFSGTHIL-TAPFLGALGIYSLSHTEVGAVPRFSTKPL 861
 Db 231 FFNNHTVLASL--DCTFLPARITRTLEQPFISAIALURCSQASFOETGDIRKPHKPL 288
 QY 862 INVLPVIGKSGFMNATORPQAWTVELAYQPVLYROEPGIATOLLASKGIWFGSGSPSR 921
 Db 289 TDLSSPGFSEKWKTHHIMLWTEISYVPTLYRKKNPEMFTLLILNSGWTQTQATPVSY 348
 QY 922 HAMSRYKTSQOTQPLSWTLHFQYHGFYSSSTFCNLYNGE 960
 Db 349 NSVAAKIKNTSQLFSRVTLSLDYSAQVSSSTVGOLKAE 387
 RESULT 7
 Q8VU50 ID Q8VU50 PRELIMINARY; PRT; 700 AA.
 AC Q8VU50;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DE Putative polymorphic membrane protein (Fragment).
 OS Chlamydia psittaci (Chlamydia psittaci).
 OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
 OX NCBI_TaxID=83554;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=POS;
 RA Laroucau K., Souriau A., Rodolakis A.;
 RT "Isolation of a new pmp sequence and evidence of pmp polymorphism in
 RT serotype-1 Chlamydia psittaci strains";
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF243415; AAL36959.1;
 DR InterPro: IPR003368; Chlamydia_PMP.
 DR InterPro: IPR003357; OMP.
 DR Pfam: PF02415; DUF145; 1.
 DR Pfam: PF02385; OMP; 1.
 FT NON_TER 700 700
 SQ SEQUENCE 700 AA; 74200 MW; 2C38E504AF48D1D1 CRC64;
 Query Match 9.4%; Score 477; DB 2; Length 700;
 Best Local Similarity 25.3%; Pred. No. 7.5e-20;
 Matches 201; Conservative 109; Mismatches 264; Indels 220; Gaps 40;
 QY 1 MKKAFFFLIGNSLGLAREVPSRIFLPMNSV--PDPTKESLSNKISLTGDTNLTNLYL 58
 Db 1 MKHPVYWFLLSSSL-----LASNSLSPAQVTNETLTSSDSYNG---NVT----- 41
 QY 59 DNLRYLAILQKTPNEGAAVTITDYSFDTQKEGIYFAKNLTPESCGAGIYASNPSTV 118
 Db 42 -----SDEFVKETTSGLIY-----TCEGNVCISYAGKDSPL- 73
 QY 119 EIRDTIGPVIFENNTCCRPETSSNPNAVNKIREGGAIHAQNLNINHVDVGVGFMKFSY 178
 Db 74 -----NKSCFSETT-----ENLSF 87
 QY 179 VRGGAISTANTFVYSENQSCFLFMDNICIQTNTAGKGAI-YAGTNSFESNCDLFFIN 237
 Db 88 IGNG-----YTLCF---DNI---TTTASNGAINVSDQKTLNVSGFSLESCA 129
 QY 238 NACCAG-----GAIFSP-ICSLTGNRGNIVYNNRCFNKVFETASSEADSGAIVTT--- 288
 Db 130 H-CPPGTGTGYGAIQTGKGVSTFSGN--NKLIFDNCC-----STGEGGAIRCATGSNA 177
 QY 289 RLDVGTNRGRIFRIFSDNITKNYGGAIYAPVTVLDVNGPTFYINN---IANKKGAIYIDGT 345

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Db 178 ELKLEGN-SYVVFSGNSSOKKGAIVTKLITADGPTLFSNNVSASSSPKGAICLDDT 236
QY 346 SNS-KISADRHAIIPENIVTNANGTSTANPPRRNAITVASSSGEILLGAGSSQNL 404
Db 237 SSECSTANIGDLTFDGN---KVIKNGGSSTV---KRNAIDLGSGGKFTKLNAGEFGI 290
QY 405 IFYDPIEVSNAGVSVSFNK-EAD--OTGSVVFSGATVNSAD-PHQRLNLOTKTPAPLTLN 460
Db 291 FFHDPIANTGGSTIEIENKTESDTTGTGKVFSGEKLSDDEEKVTPNKLKSYFKQPKIKGA 350
QY 461 GFICIEDHQAOLTVNRQTQ--GGVSLGNGAVLSCYKNGAGNSASNAITLKHIGLNLSS 519
Db 351 GSVLVDGVTLEAKKITQTKGTSVVMDLGTLTQT-----PSSSGETITLNLNDINIASL 404
QY 520 LKSGAEIPLLWVEPTNNSNYTADTATFSLSDVKLSLIDDYGNSSYESTDLTHALSSQP 579
Db 405 GGGGGTAPA-----KLATNTASQAISIAAVALNVTDSNT-YE-----DP 442
QY 580 MLSISA-----SDNQLRSDMDDFSGLINVP-HYGWQGLMTGWAKTQDPEPASATI 630
Db 443 ILSASKSFAITATTSSSTVTPPETNLKNYTPPTHYGYOGNWTLW-----PPGETMQL 496
QY 631 TDPQKANRRHRTLWLPAGYVPSPKRHSPLIANTLWGNM--LLATESLK-----NSAEL 684
Db 497 -----KTATLNWEOGTGYSNPERVGSVLPNTLWGSFSDIRAIQNLMDVSVNGADY 546
QY 685 TPSDHPFWGITGGGLGMVYQDPRENHGFHMRSSGYSAGMIAGTQHT---PSLKFSQY 741
Db 547 S---RGFW---VSGLANFLNKSQSDTKRFRHNSAGYALGVYA-QTPSEDIFFSAFCOLF 599
QY 742 TKLNERYAKNNVSS 755
Db 600 GRDKDYFLSKNSST 613

RESULT 8
QYRB61
ID QYRB61 PRELIMINARY; PRT; 347 AA.
AC QYRB61;
DT 01-MAY-2000 (TremBLrel. 13, Created)
DT 01-OCT-2000 (TremBLrel. 15, Last sequence update)
DE 01-JUN-2002 (TremBLrel. 21, Last annotation update)
DE Polymorphic outer membrane protein.
GN PMP_17.2.
OS Chlamydia pneumoniae (Chlamydia pneumoniae).
OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxID=83558;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=J138;
RX MEDLINE=20330349; PubMed=10871362;
RA Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K.,
RA Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.;
RT "Comparison of whole genome sequences of Chlamydia pneumoniae J138
RL from Japan and CWL029 from USA.";
RL Nucleic Acids Res. 28:2311-2314(2000).
DR EMBL: AP002546; BAA98675.1;
DR InterPro: IPR003368; Chlamydia_pmp.
DR Pfam: PF02415; DUF145; 1.
SQ SEQUENCE 347 AA; 37314 MW; 8A62367A2664972A CRC64;
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Query Match 8.3%; Score 422; DB 16; Length 347;
Best Local Similarity 32.4%; Pred. No. 47e-17;
Matches 110; Conservative 56; Mismatches 151; Indels 22; Gaps 7;

QY 246 IFSPICSTGNRGNTVFNVRCKNVETASSEASDGGAIKVTRLDVTGNRGRIFFSDNI 305
Db 1 MFSALGVITSSNKEIETSNHSASSINTASGLKYPGGGIMCTSLVIENPKGLIFNKT 60
QY 306 TKNYGGAIYAPVTVLDNGPYTFINNIANNKGAIYIDG-----TSNKSISADRHAIINE 361
Db 61 AALSGGAIHTRSFIFQNGPTAFINNSATSGALINLSIGISTPONFFLSADYGDILFNN 120
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QY 362 NIYVNTVNGTSTANPPRRNAITVASSSGEILLGAGSSQNLIFYDPIEVSNAGVS-VS 420
Db 121 NNT-----TSSSPQGYRNAL-YAAPGINLKLGAROGYKILFYDPIHDQTTDPIV 171
QY 421 FNKEADQTSVVFSGATVNSADPHQRLNLOTKTPAPLTLNSNGFLCIEDHQAOLTVNRFTQTG 480
Db 172 FNYEPHLLGTVLFSGINVDNATNPLNLSKFSNSSLRGVLAIEDRAISCKTLSQTG 231
QY 481 GVVSLGNGAVLSCYKNGAGNSASNAITLKHIGLNLSSILKSGAEIPLWVEPTNNSNY 540
Db 232 GILRLGNAALIR--TRGPG-----SSINFNATAINLPSILQSEASAPKFWIYPTLTGSTY 284
QY 541 TADTATFSLSDVKLSLIDDYGNSSYESTDLTHALSSQP 579
Db 285 SEDTSTITLSG-PLTFLNDENENPYDLSLSEPRKDIP 322

RESULT 9
QY3QEB
ID QY3QEB PRELIMINARY; PRT; 1530 AA.
AC QY3QEB;
DT 01-DEC-2001 (TremBLrel. 19, Created)
DT 01-DEC-2001 (TremBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TremBLrel. 21, Last annotation update)
DE Cytolysin.
GN CTC.
OS Chlamydia trachomatis.
OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxID=813;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=434/BU;
RA Lampe M.F., Ballweber L.M., Johnson M.L., Kiselev A.O., Yates J.R.,
RA Stamm W.E.;
RT "Cloning and analysis of ctc, a putative cytolysin and member of a
RL multigene family from Chlamydia trachomatis serovar L2.";
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF268092; AAK69391.1;
DR InterPro: IPR003368; Chlamydia_pmp.
DR InterPro: IPR001899; Gram_pos_anchor.
DR InterPro: IPR003357; OMP.
DR InterPro: IPR000531; TonB_boxC.
DR Pfam: PF02415; DUF145; 1.
DR Pfam: PF02385; OMP; 1.
DR PROSITE: PS00343; GRAM_POS_ANCHORING; UNKNOWN1.
DR PROSITE: PS00430; TONB_DEPENDENT_REC_1; UNKNOWN1.
SQ SEQUENCE 1530 AA; 160459 MW; F9FCE3F8EF9A89F CRC64;
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Query Match 7.6%; Score 387; DB 2; Length 1530;
Best Local Similarity 20.5%; Pred. No. 4e-14;
Matches 287; Conservative 140; Mismatches 422; Indels 552; Gaps 63;

QY 7 FFLIGNSLGLAREVPSRIFLMPNSVDPDTKESLNKISLTGDTNLTN-----C 56
Db 240 FFWTG-SLSG-----EKSLYMP--AGDMVAVMCDGAISEFGNSANFANGAIAASGKVL 290
QY 57 YLDNLRYILAILQKTPNEGAATITDYSLFFDTQK----- 91
Db 291 FVANDKK-TSFTEINRALSAGAIASAASDIAFQNCALVFKNGCAIGTEDKSLGGGAISL 349
QY 92 -----EGYVFAKNLTPESGGAIGYASPNSTPTEIRDTIGPVFENNTCCRPFTSSNP 143
Db 350 GTVLLQGNHIGTCDKNESASQGGAI-----FGKNCQISDNEGVPVFRSTAC----- 396
QY 144 NAAVNKIREGGAIAHQNLY-INNHHDVVGF-----MKNFSYVRG----- 181
Db 397 -----LGGGAIAAQAEIVSIQNNAGISFEGGKASFGGGIACGSFSSAGGASVLGTIDI 449
QY 182 ----CAISTANTFV-----VSENQSCFLFMONICITQTTAGK- 214
Db 450 SKNLGAISFSRSLCTCTSDLGOMEYOGGALFGENISLENAGVLTFKONIVKTFASNGKI 509
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QY 215 --GGAIYAGTSNFSFNCDLFFINNA-----239
|||||:|:|:|
Db 510 LGGGAILATGKVEITNNSGGISFTGNARAPQALPTQBEFFLFKSKKEGRPLSSGYSGGAI 569
QY 240 -----CCAGGAIFS-PICSLTGNRGNIVFYNNRC 267
|||:|:|:|
Db 570 LGREVALHNAVVFQONRLQCSEEAATLGGCCGGAVHGMGSTIVGN-SSVRFNGNYA 628
QY 268 F-----KNVETASSEAD-----GGAIKVT-----287
|||:|:|:|
Db 629 MGQGVSGALLSKTVQLAGNSVDFSGNIASLGGALQASEGNCELVDNGYVLFDRNRR 688
QY 288 -----TRLDV-TGNRGRIFSDNI-TKNY-----309
|||:|:|:|
Db 689 VYGAISCLRGDVIISGNKGRVEFKDNIAIRLYVEETVEKVEEPAEQKDNNELSFLG 748
QY 310 -----GGAIYAPVTVLVDN-GPTYF 328
|||||:|:|:|
Db 749 SVFQSFITANQALFASDGLSPSSISSEELAKRRECCAGGAIFAFAKRVIRVDNQEAUVF 808
QY 329 INNIAANKGCAIYIDG-TSNSKISADRHAIIFENIVTVNTNANGTSTSANPPRRNAITV 387
|||:|:|:|
Db 809 SNFSDIYGGAITGSLREEDKLDGQIPEVLISGNAGDVVFSGNSKRDEHLPTGGGAI 868
QY 388 ASSSGEILLGAGSSQNLIFYDPIEVSNAVSV-----SFNKAD 426
|||:|:|:|
Db 869 CTQNLRTISQWTG--NVLFYNNVACSGGAVRIEDHGNVLEAFGGDIVFKGNSF--RAQ 923
QY 427 QTSVVFSG-----ATVNSAD-----FHQ-----RNLQTKTPAPLTLSNG-----461
|||:|:|:|
Db 924 GSDAIYFAGKESHITALNATEHAIVFDALVFENLKERKSAEVLNLSRENPGYTGSR 983
QY 462 FL-----CIEDHAQLTVNRQTGGVYSLGNGAVLSY--KNGAGNS--ASNASIT 508
|||:|:|:|
Db 984 FLEAESKVPQCI--HWQ-----QGSLELLNGATLCSYGKQDAGAKLVLAAGSKL 1032
QY 509 LKHIGLNL--SILKGAETP-----LWVE-----PTNNSNNYTDATATFSL 550
|||:|:|:|
Db 1033 ILDSGTPVOGHAIKSEPAEIESSEPEGAHSLWIAKNAQTVPWVHIHTISVD-LASFSS 1091
QY 551 S-----DVKLSLIDDYGNSPYESTDTHALSSOPMLSSISASD 588
|||:|:|:|
Db 1092 SOOEGTVEAPQDIVPGGYSVRSGELNLELVNTTGTG-YENHALLKNEAKVPLMSFVASSD 1150
QY 589 NOLRSDMDPFGSLNVPH-----YGNQGLWTGWAKTQDPEPASSATITDPQ 634
|||:|:|:|
Db 1151 EA-----SAEISNVSQDLQIHVATPEIETDYGHMG--DWSEAKIQD-----1191
QY 635 KANRFRHTLLTLWLPAGYVPSPKHRSPLIANTLW--GNMLLATESLKNSAELTPSDHPF- 691
|||:|:|:|
Db 1192 -----GTLVINNNPTGYRLDPQKAGALVFNALWEEGAVLSALKNARFAHNLTAQRMEFD 1245
QY 692 -----RGITGGGLGMVYQDPREN---HPGFHRSSGYSAGMTAGOTHFSLFQSQT--Y 741
|||:|:|:|
Db 1246 YSTNVMGFAFGPRTL-----SAENLVAIDGYKAGYASAGVDIQLMEDEVLGYSAAFL 1301
QY 742 TKLNERYAKNNVSKNYSKOGEMLFSLQEGFLTK-LVGLSYGDNHCHHFYTOGENLT 799
|||:|:|:|
Db 1302 GRMDSOKFDEVRKKG-----VVGSVYTGFLAGSWFFRQYSLGE-----TQNDMKT 1348
QY 800 SQGT-----RSQTMGGAV-----FFDLPMKPFSGTHILTAFLGALGI 838
|||:|:|:|
Db 1349 RYGLVCESSASWT-SRGVLADALVEYSLVCPVRPTFYALHFNFYVEVSYASMKFPG----1404
QY 839 YSSLSHFTEVGAYPRSFSTKPTLINLVPTG-----VKGSP--MNATORPOAWTVELA 889
|||:|:|:|
Db 1405 -----FTEQGREARSFEDAS-LTNITPLGMKRFELAFIKQGFSEVNSLGISYAWEA---1454
QY 890 YQPVLYRQEGIAQTALLAKGIFWGSPPSSRRHMSYKISQQTQPLSW-----LTLHFQYH 945
|||:|:|:|
Db 1455 -----YRKVBGGAVQLLEAGFDWEGAPMDLPROELRVALENNTWSSYFSTVLGLTAFCG 1509
QY 946 GFYSSTFCNY-LNGEIALRF 965
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Db 1510 GFTSTDSKLGYEANAGRLRIF 1530
|||:|:|:|

RESULT 10
Q8VU49
ID Q8VU49 PRELIMINARY; PRT; 602 AA.
AC Q8VU49;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Putative polymorphic membrane protein (Fragment).
OS Chlamydia psittaci (Chlamydotheca psittaci).
OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydotheca.
NCBI_TaxID=83554;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=LLG;
RA Laroucau K., Souriau A., Rodolakis A.;
RT "Isolation of a new pmp sequence and evidence of pmp polymorphism in
RT serotype-1 Chlamydia psittaci strains.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF243418; AAL36962.1; -.
DR InterPro; IPR003368; Chlamydia_PMP.
DR InterPro; IPR003357; OMP.
DR Pfam; PF02415; DUF145; 1.
DR Pfam; PF02385; OMP; 1.
DR NON_TER 1
FT NON_TER 1
SQ SEQUENCE 602 AA; 65562 MW; CA486CFACEC131E2 CRC64;

Query Match 6.9%; Score 349; DB 2; Length 602;
Best Local Similarity 25.3%; Pred. No. 1.9e-12;
Matches 167; Conservative 97; Mismatches 261; Indels 136; Gaps 36;

QY 357 IIFNEN-IVTVNTNANGTSTSANPPRRNAITVASSSGEILLGAGSSQNLIFYDPI-EVSN 414
|||:|:|:|
Db 4 ITFDGNKIIT-----TSRSSSTVTKRNSISLGGGRTKLNAKEGFIFFDPIANTGD 56
QY 415 AGVSVSENK-----EADOTGSVVFSGATVNS-----ADFHORNLOTKTPAPLTLSNGFLCI 465
|||:|:|:|
Db 57 TNEIELNKAEGSTTYTGKIVFSGEKLDEKKVAD-----NLKSYFTQPLKAGAGSLVL 112
QY 466 EDHAQLTVNRFTOT-GGVVSLGNGAVLSYKNGAGNSASNASITLKHIGLNLSSILKSGA 524
|||:|:|:|
Db 113 KDGVTLEAKVSDQSTGVVMDLGTTLQ-----TSSGETITLNLIDINVASLGGGV 165
QY 525 EIPLLWVPTNNNNYNTADTAFTSLSDVKLSLIDDYGNSPYESTDTHALSSOPMLSS-I 583
|||:|:|:|
Db 166 APDPKAVEAQASGKTVTINA-----VNLVDTDGNA-YEYPILA--TSQPTAII 211
QY 584 SEASDNLQRSDDDFSLNVP--HYGWOGLWTGWAKTQDPEPASSATITDPKANRFRH 641
|||:|:|:|
Db 212 AKAGSGSTTTPTDNLKNYTPPTHYGYGNWTVTW-----KLGTSAQ-----EE 255
QY 642 TLLTLTPAGYVPSPKHRSPLIANTLWGNM--LLAVTESL-----KNSAELTPSDHPFWGIT 695
|||:|:|:|
Db 256 TAILTWEQDYSNPERQGLVPNTLWGSFSDIRAQLNLDISVNGADYR--RGFW---309
QY 696 GGGGLGMVYQDPRENHPGFHRSSGYSAGMIAGOTHF--FSLKFSQTYTKLNERYAKNN 752
|||:|:|:|
Db 310 VSLGFLNPLKSGSNTRKFRHSHSAGVALGYA-QTSTEDVFSAAFCLFGKDKDYFVSKN 368
QY 753 VSKNYSKOGEMLF--SLQEGF--LLTKLVGL-----YSYGDHNCHEHYTOGENL 798
|||:|:|:|
Db 369 -SSNIYA--GSIYQYHISYWNWONLLQSTIGAEAPLVLAQTY-----CHASNMMKTNM 421
QY 799 TS-----OQTFRSQTMG---GAVFFDLPKM-PFGSHTILTAFLGALGYSYL 842
|||:|:|:|
Db 422 TNYVPAKNVTLSKIGDWGNDGCFEGEGAM---APIETPSSFLFDYSPFLQQLVHAHQ 478
QY 843 SHFTEVGAYPRSFSTKPTLINLVPTIGVKGFSMNATORPOAWTVELAYQPVLYRQEGIA 902
|||:|:|:|
Db 479 DDFKENNSDQGRYFESSNLTLNMPIGIKPERF-AYNDVASYHLTAAYADPDIVRSPDCT 537
```


Db 369 -SSNIYA--GSIYYQHISYNNAMONLQSTIGAEAPLVLAQLTY-----CHASNMMKTNM 421
QY 799 TS-----OQTFRSOTMG---GAVFEDLPMKPFSGTHIL---TAPFICGALGIYS 840
Db 422 TINTVPPKNVILSELKGDWDCDFVEFGA-----MAPIENASLFDPRYSFPLQLQLVHA 475
QY 841 SLSHFTVEGAYPRFSFTKTPLINVLVPIGVKGSFPMNATQRPQAWTVLQAPVLYROBPG 900
Db 476 HODDFKENNSDOGRYFESSNLTNSMPIGIKFERF-AYNDVASYHLTAAYAPDIVRSNPD 534
QY 901 IATOLLAS--KGWIFGSGSPSSRRAMSKYKISQOTQPLSWLTLH-----FQYHGFY---SS 950
Db 535 CTASLLVSPTSAVVWTKANLARSFA-----MLQAGNYLALSHNMELFSQGFGEIRGSS 588
QY 951 STF 953
Db 589 RTY 591

RESULT 13
Q9RB68 PRELIMINARY; PRT; 494 AA.
AC Q9RB68
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Polymorphic outer membrane protein G family.
GN PMP_5.1
OS Chlamydia pneumoniae (Chlamydia pneumoniae).
OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia. 494
OX NCBI_TaxID=83558;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=J138;
RX MEDLINE=20330349; PubMed=10871362;
RA Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K.,
RA Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.;
RT "Comparison of whole genome sequences of Chlamydia pneumoniae J138
RT from Japan and CWL029 from USA";
RL Nucleic Acids Res. 28:2311-2314(2000).
DR EMBL; AP002545; BAA98230.1; -;
DR InterPro; IPR003368; Chlamydia_PMP.
DR Pfam; PF02415; DUF145; 2.
SQ SEQUENCE 494 AA; 50229 MW; 5BD8A44AB3A64171 CRC64;

Query Match 6.3%; Score 321; DB 16; Length 494;
Best Local Similarity 26.0%; Pred. No. 6.2e-11;
Matches 128; Conservative 75; Mismatches 186; Indels 104; Gaps 20;

QY 33 PDPTKESLSNKISLTGDTNLTNCYLDNRYILAILQKTPNEGAATITDYLSPFDTOKE 92
Db 45 PKSTTDAAGTYSLTGEV-----LYID-----PKGGSITGT---CEVETAGD 84
QY 93 GIYFA-----KNLTPESGGAGVYAS-PNSPVEIRDTIGPVFNNTCCRPFTSSNPAA 146
Db 85 LTFGLNGNTLKLFSVDAGANIAVHVGSKNLSFTDFLSLVI-----SPKSA 133
QY 147 VN-----KIREGAIHAQNYLIHNHNDVVGFMKNFSYR 180
Db 134 VTTGKGLSLGAVQLQDINTLVLSNASVEDGKVGKNSCLIQGKNSAIFGQNTSSK 193
QY 181 GGAISTANTFVSENOQCFMDNICIOTNAGKGAIYAGTNSPESNCDLFFINNA- 239
Db 194 GGAISTTQGTIENNLTLKFNENKAVTS-----GGALDGAASTFTFANH-ELIFSQNT 247
QY 240 ---CCAGGAIPTCSLTGRGNIVFYNNRCFNKVTETASSEADGGAIKVTTRLDVTGNR 296
Db 248 SGNAANGAI--NCS-----GDLTFDNTSLLLQE---NSTMQDGCALCSTGISITGS- 296
QY 297 GRIFFSDNITKNYGGAIYAPVVTLV-DNGPTYFINNI---ANNKGGAIYIDGTSNKSISA 352
Db 297 DSINVIGTSGQGGAIASAASLKGOGGALFSNNVVTHATPLGGAIFINTGSLQFT 356

QY 353 DRHAIIFENIVTNTNANGTSTSANPRRNATVASSSGEILGAGSSQNLIIFYDPIEV 412
Db 357 OGGDIVEGNOVT--TAPNATT-----KRNVIHLESTAKWTGLAASOGNAIFYDPIIT 409
QY 413 SNAGVS-----VSFNKEADQTSVFSGATVNSADFHQNLQTKTPAPLTLSNGELCI 465
Db 410 NDTGASDNLRLINEYASQKL--SGSIVFSGERLSTAEIAENLTSRINQPVTLVEGSLVL 467
QY 466 EDHAQLTVNRFTQ 478
Db 468 KQGVTLITQGSQ 480

RESULT 14
Q9RB70 PRELIMINARY; PRT; 427 AA.
AC Q9RB70
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Polymorphic outer membrane protein G family.
GN PMP_4.1
OS Chlamydia pneumoniae (Chlamydia pneumoniae).
OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia. 427
OX NCBI_TaxID=83558;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=J138;
RX MEDLINE=20330349; PubMed=10871362;
RA Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K.,
RA Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.;
RT "Comparison of whole genome sequences of Chlamydia pneumoniae J138
RT from Japan and CWL029 from USA";
RL Nucleic Acids Res. 28:2311-2314(2000).
DR EMBL; AP002545; BAA98227.1; -;
DR InterPro; IPR003368; Chlamydia_PMP.
DR Pfam; PF02415; DUF145; 1.
SQ SEQUENCE 427 AA; 43419 MW; AB4BBBC1594DD2B1 CRC64;

Query Match 5.8%; Score 297; DB 16; Length 427;
Best Local Similarity 30.0%; Pred. No. 1.3e-09;
Matches 119; Conservative 47; Mismatches 121; Indels 110; Gaps 18;

QY 61 LRYILAILQKTPNEGAATITDYLSPFDTOKEGIYFAKNLTPESSGGAIYASPNPTVEI 120
Db 130 LRMLAA--PRTTGGK-AIKITDGLVF--ESIGNLDLNEASSENCGAI-----NFKLSL 179
QY 121 RDTIGPVIFENNTCCRPFTSSNPAAVYKIREGAIHAQ-NLYIHNHNDVVGFMKNFSYV 179
Db 180 TGSPTFVAFNGN-----SSSQGGAIYASGDSVISENAGILSFGNNSATT 224
QY 180 RGAISTANTFVSENOQCFMDNICIOTNAGKGAIYAGTNSPESNCDLFFINNA 239
Db 225 SGGAIASAGNLVLSNNQN--IFFDGCKATTN-----GGAI-----D 258
QY 240 CCAGGAIPTCSLTGRGNIVFYNNRCFNKVTETASSEADGGAIKVTTRLDVTGNRGI 299
Db 259 CNKAGANPDILLUSGNE-SLHFLNN-----TAGNSGGAI-YTKKLVLSSGGRGV 306
QY 300 FFSNITKNYGGAIYAPVVTLVNDNGPTYFINNIANNKGGAIYIDGTSNKSISADRAHAIIF 359
Db 307 LFSNNKAAN-----ATPKGGAIALDSGEISISADLGNIIIF 342
QY 360 NENIVTNTNANGTSTSANPP--RRNAITVASSSGEILGAGSSQNLIIFYDPIEVSNAGV 417
Db 343 -----EGNTTSTGSPASVTRNAIDLASNAKFLNLRATRGKVIIFYDPIITSSGATD 393
QY 418 SVSFNKEAD-----QTGSVVFSGATVNSADFHQNL 448
Db 394 KLSLNK-ADAGSGNTYEGYIVFSGEKLSEV-----RNL 425

RESULT 15

Search completed: February 4, 2003, 20:57:49
Job time : 101 secs

GenCore version 5.1.1.3
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OM protein - protein search, using sw model

Run on: February 4, 2003, 19:10:17 ; Search time 40 Seconds
(without alignments)
1000.616 Million cell updates/sec

Title: US-09-677-752-2
Perfect score: 5086
Sequence: 1 MKKAPFFFLIGNSLGLARE.....GFYSSSTFCNLYNGEIALRF 965

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	4389.5	98.1	964	1 PMPE_CHLTR	O64877 chlamydia t
2	3648.5	71.7	976	1 PMPE_CHLMO	O9p147 chlamydia m
3	1120.5	22.0	938	1 PM15_CHLPN	O9z883 chlamydia p
4	1060.5	20.9	952	1 PM16_CHLPN	O9z882 chlamydia p
5	951.5	18.7	946	1 PM18_CHLPN	O9z880 chlamydia p
6	866.5	17.0	1034	1 PMPE_CHLTR	P38008 chlamydia t
7	793	15.6	1025	1 PMPE_CHLMO	O9p146 chlamydia m
8	655.5	12.9	1013	1 PMPG_CHLTR	O64879 chlamydia t
9	644	12.7	936	1 PMP7_CHLPN	O9z898 chlamydia p
10	620.5	12.2	987	1 PMPG_CHLMO	O9p145 chlamydia m
11	617	12.1	930	1 PMP8_CHLPN	O9z393 chlamydia p
12	597	11.7	928	1 PM11_CHLPN	O86164 chlamydia p
13	595	11.7	1016	1 PMPH_CHLTR	O84880 chlamydia t
14	586.5	11.5	928	1 PM10_CHLPN	O9rb65 chlamydia p
15	586	11.5	947	1 PM19_CHLPN	O9z813 chlamydia p
16	585.5	11.5	928	1 PMP9_CHLPN	O9z398 chlamydia p
17	583	11.5	978	1 PM14_CHLPN	O9z895 chlamydia p
18	575	11.3	973	1 PM13_CHLPN	O9z896 chlamydia p
19	570.5	11.2	922	1 PMPL_CHLPN	O9z965 chlamydia p
20	567	11.1	1276	1 PMP6_CHLPN	O9z899 chlamydia p
21	564	11.1	980	1 PMPH_CHLMO	O9p144 chlamydia m
22	546.5	10.7	976	1 PMPA_CHLMO	O9pjy3 chlamydia m
23	525.5	10.3	841	1 PMP2_CHLPN	O9z3a1 chlamydia p
24	519.5	10.2	975	1 PMPA_CHLTR	O84417 chlamydia t
25	517	10.2	1723	1 PM20_CHLPN	O9z812 chlamydia p
26	474.5	9.3	1609	1 PM21_CHLPN	O9z605 chlamydia p
27	470.5	9.3	878	1 PMPI_CHLTR	O84882 chlamydia t
28	457	9.0	867	1 PMPI_CHLMO	O9p141 chlamydia m
29	395	7.8	1754	1 PMPB_CHLTR	O84418 chlamydia t
30	389.5	7.7	1672	1 PMPB_CHLMO	O9pjy2 chlamydia m
31	386	7.6	1531	1 PMPD_CHLTR	O84818 chlamydia t
32	377.5	7.4	1460	1 PMPC_CHLMO	O9pjy1 chlamydia m
33	358.5	7.0	1520	1 PMPD_CHLMO	O9p1b0 chlamydia m

ALIGNMENTS

RESULT 1				
PMPE	CHLTR	STANDARD;	PRT;	964 AA.
ID	PMPE_CHLTR			
AC	O84877;			
DT	30-MAY-2000 (Rel. 39, Created)			
DT	30-MAY-2000 (Rel. 39, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Probable outer membrane protein pmpe precursor (Polymorphic membrane protein E).			
DE	protein E).			
GN	PMPE OR CT869.			
OS	Chlamydia trachomatis.			
OC	Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.			
OX	NCBI_TaxID=813;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=D/UW-3/Cx;			
RX	MEDLINE=99000809; PubMed=9784136;			
RA	Stephens R.S., Kalman S., Lammel C.J., Fan J., Marathe R., Aravind L.,			
RA	Mitchell W.P., Olinger L., Tatusov R.L., Zhao Q., Koonin E.V.,			
RA	Davis R.W.;			
RT	"Genome sequence of an obligate intracellular pathogen of humans:			
RT	Chlamydia trachomatis."			
RL	Science 282:754-759(1998).			
CC	-1- SUBCELLULAR LOCATION: CELL WALL SURFACE (ELEMENTARY BODIES)			
CC	(POTENTIAL).			
CC	-1- SIMILARITY: BELONGS TO THE PMP OUTER MEMBRANE PROTEIN FAMILY.			
CC	-----			
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@isb-sib.ch).			
CC	-----			
DR	EMBL: AE001360; AAC68467.1; -			
DR	InterPro: IPR003368; Chlamydia_PMP.			
DR	InterPro: IPR003357; OMP.			
DR	Pfam: PF02385; OMP; 1.			
DR	Pfam: PF02415; DUF145; 1.			
KW	Outer membrane; Signal; Multigene family; Complete proteome.			
FT	SIGNAL 1 18 POTENTIAL.			
FT	CHAIN 19 964 PROBABLE OUTER MEMBRANE PROTEIN PMPE.			
SQ	SEQUENCE 964 AA; 104703 MW; 1B998A7D2E57ICE2 CRC64;			

Query Match		98.1%	Score 4989.5;	DB 1;	Length 964;
Best Local Similarity		98.3%	Pred. No. 4.7e-306;		
Matches 949;		Conservative 7;	Mismatches 8;	Indels 1;	Gaps 1;
QY	1 MKKAPFFFLIGNSLGLAREVPSRIFLMPNSVDPPTKESLSNKISLFGDTHNLTNCLDN 60				
Db	1 MKKAPFFFLIGNSLGLAREVPSRIFLMPNSVDPPTKESLSNKISLFGDTHNLTNCLDN 60				
QY	61 LRYTLAIQKTPNEGAATTTDYLSTFDQKEGIYFAKNLTPESGGAIGVASPSTVEI 120				
Db	61 LRYTLAIQKTPNEGAATTTDYLSTFDQKEGIYFAKNLTPESGGAIGVASPSTVEI 120				

O84419 chlamydia t
O9z3d6 chlamydia p
P45508 escherichia
Q52657 rickettsia
Q53020 r outer mem
P96989 r outer mem
P14914 rickettsia
O53047 r outer mem
O06653 r outer mem
P33666 escherichia
P15921 rickettsia
O9kka3 r outer mem

QY	121	RTDITGVIFENNTCCRPFTSSNPNAVNKIREGGAHAQONLYINHHNDVVGVGMKNEFSYVR	180
DB	121	RTDITGVIFENNTCCRLFTWRNPYAA-DKIREGGAHAQONLYINHHNDVVGVGMKNEFSYVQ	179
QY	181	GGAISTANTFVVENSCSFLFMDNICIQNTAGKGAIACTSNESNCDLFFINNAC	240
DB	180	GGAISTANTFVVENSCSFLFMDNICIQNTAGKGAIACTSNESNCDLFFINNAC	239
QY	241	CAGGAIFSPICSLTGNRGNIYVNNRCFKNVETASSEASDGGAIKVTTRDLVTGNRGRIF	300
DB	240	CAGGAIFSPICSLTGNRGNIYVNNRCFKNVETASSEASDGGAIKVTTRDLVTGNRGRIF	299
QY	301	FSDNITKNGGAIYAPVTVLVONGPYFINNIANNKGAIYIDGTSNSKISADRHAIIFN	360
DB	300	FSDNITKNGGAIYAPVTVLVONGPYFINNIANNKGAIYIDGTSNSKISADRHAIIFN	359
QY	361	ENIVTNVNTANGTSTSANPPRNAITVASSSGEILLGAGSSQNLIIFYDPIEVSNAGVSYS	420
DB	360	ENIVTNVNTANGTSTSANPPRNAITVASSSGEILLGAGSSQNLIIFYDPIEVSNAGVSYS	419
QY	421	FNKEADOTGSVVFSGATVNSADFHORNLOTKTPAPLTLSNGFLCIEDHAQLTWNRTQTG	480
DB	420	FNKEADOTGSVVFSGATVNSADFHORNLOTKTPAPLTLSNGFLCIEDHAQLTWNRTQTG	479
QY	481	GVVSLGNGAVLSYKNGAGNSASNATILKHIGLNLSSILKSGAEIPLLWVEPTNNSNY	540
DB	480	GVVSLGNGAVLSYKNGAGNSASNATILKHIGLNLSSILKSGAEIPLLWVEPTNNSNY	539
QY	541	TADTAATFSLSDVKLSLIDDYNSPYESTDLTHALSSQPMLSISASDNQLRSDMDFFSG	600
DB	540	TADTAATFSLSDVKLSLIDDYNSPYESTDLTHALSSQPMLSISASDNQLRSDMDFFSG	599
QY	601	LNVPYHGWGLTWGAKTQDPEPASSATITDPOKANRHFRTLLTLWLPAGVVPSPKHRS	660
DB	600	LNVPYHGWGLTWGAKTQDPEPASSATITDPOKANRHFRTLLTLWLPAGVVPSPKHRS	659
QY	661	PLIANTLWGNMLLATESLKSNAELTSPDHPFWGITGGGLGMVYQDPRNHPGFHMRSSG	720
DB	660	PLIANTLWGNMLLATESLKSNAELTSPGHPFWGITGGGLGMVYQDPRNHPGFHMRSSG	719
QY	721	YSAGMAGQTHYFSLKFSQTYTKLERYAKNNVSKNYSQCQEMFLFSQEGELLTKLVGL	780
DB	720	YSAGMAGQTHYFSLKFSQTYTKLERYAKNNVSKNYSQCQEMFLFSQEGELLTKLVGL	779
QY	781	YSYGDHNCHEFTQENLTSCQTFERSQTMGGAVFEDLPMKPGSTHILTAPFLGALGIYS	840
DB	780	YSYGDHNCHEFTQENLTSCQTFERSQTMGGAVFEDLPMKPGSTHILTAPFLGALGIYS	839
QY	841	SLSHTEVGAYPRSFSTKTPLINLVPIGVKGSEFNATQRPQAWTVELAYQPVLYRQEPG	900
DB	840	SLSHTEVGAYPRSFSTKTPLINLVPIGVKGSEFNATQRPQAWTVELAYQPVLYRQEPG	899
QY	901	INTOLLASKGIWFGSGSPSSRRAMYSKISQQTQPLSWLTLHPQYHGFYSSSTFCNYLNGE	960
DB	900	IAAQLLASKGIWFGSGSPSSRRAMYSKISQQTQPLSWLTLHPQYHGFYSSSTFCNYLNGE	959
QY	961	IALRF 965	
DB	960	IALRF 964	
RESULT 2			
PMPE_CHLMU			
ID	PMPE_CHLMU	STANDARD;	PRT; 976 AA.
AC	O9PL47:		
DT	16-OCT-2001 (Rel. 40, Created)		
DT	16-OCT-2001 (Rel. 40, Last sequence update)		
DE	16-Oct-2001 (Rel. 40, Last annotation update)		
DE	Probable outer membrane protein pmpE precursor (Polymorphic membrane protein E).		
GN	PMPE OR TC0261.		
OS	Chlamydia muridarum.		

OC	Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.		
OX	NCBI_TaxID=83560;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=MoPn / Nig9;		
RX	MEDLINE=20150255; PubMed=10684935;		
RA	Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,		
RA	White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S.,		
RA	Linher K., Weldon J., Khouri H., Craven B., Bowman C., Dodson R.,		
RA	Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.,		
RA	Eisen J., Fraser C.M.;		
RT	"Genome sequences of Chlamydia trachomatis MoPn and Chlamydia		
RT	pneumoniae AR39.";		
RL	Nucleic Acids Res. 28:1397-1406(2000).		
CC	-!- SUBCELLULAR LOCATION: CELL WALL SURFACE (ELEMENTARY BODIES)		
CC	(POTENTIAL).		
CC	-!- SIMILARITY: BELONGS TO THE PMP OUTER MEMBRANE PROTEIN FAMILY.		
CC	-----		
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/		
CC	or send an email to license@isb-sib.ch).		
CC	-----		
DR	EMBL; AE002293; AAF39130.1; -		
DR	TIGR; TC0261; -		
DR	InterPro; IPR003368; Chlamydia_PMP.		
DR	InterPro; IPR003357; OMP.		
DR	Pfam; PF02385; OMP; 1.		
DR	Pfam; PF02415; DUF145; 1.		
KW	Outer membrane; Signal; Multigene family; Complete proteome.		
FT	SIGNAL 1 18 POTENTIAL.		
FT	CHAIN 19 976 PROBABLE OUTER MEMBRANE PROTEIN PMPE.		
FT	SEQUENCE 976 AA; 105964 MW; 0BEA56158E3CEEA9 CRC64;		
Query Match			
Best Local Similarity 70.5%; Score 3648.5; DB 1; Length 976;			
Matches 689; Conservative 121; Mismatches 154; Indels 13; Gaps 3;			
QY	1	MKKAFEFFFLIGNSLGLAREVPSRIFLMPNSVPDPTKESLSNKISLTGTHNLTCYLDN	60
DB	1	MKKLEFFFLIGSILGFTREVPPSILLKPLNPHYMTGLFFPKVNLGTHNLTOYHLDN	60
QY	61	LVYILAILOKTNEGAATITDYLSEFFDQKEGIYFAKNLTPESGAGCIYASNPSTVEI	120
DB	61	LKCIILACIORTDYEGAATFTDYLGLFSDTKDGIKFCFKNLTPESGGVIGSPQNTPTIKI	120
QY	121	RDITGVIFENNTCCRPFTSSNPNAVNKIREGGAHAQONLYINHHNDVVGVGMKNEFSYVR	180
DB	121	HNTIGPVLFFENNTCHRLWTQTDPENEGNAKREGGAIHAGDVYISNNQNLGVIKNFAYVQ	180
QY	181	GGAISTANTFVVENSCSFLFMDNICIQNTAGKGAIACTSNESNCDLFFINNAC	240
DB	181	GGAIS-ANTFAYKENKSSFLCLNNSCIQTKTGKGAIVYSTSCSFENNKKDLFTQNSG	239
QY	241	CAGGAIFSPICSLTGNRGNIYVNNRCFKNVETASSEASDGGAIKVTTRDLVTGNRGRIF	300
DB	240	CAGGAIFSPICSLTGNRGNIYVNNRCFKNVETASSEASDGGAIKVTTRDLVTGNRGRIF	299
QY	301	FSDNITKNGGAIYAPVTVLVONGPYFINNIANNKGAIYIDGTSNSKISADRHAIIFN	360
DB	300	FSDNISRNFEGGAIHAPCLHVLGNGPYFTNNIANTHGGAIYITGTETSKISADHAIIFD	359
QY	361	ENIVTNVNTANGTSTSANPPRNAITVASSSGEILLGAGSSQNLIIFYDPIEVSNAGVSYS	420
DB	360	NNISANTNADGSSNTNPPHNRNATIMONSAGGIELGAGKSNLIIFYDPIQVTNAGVTVD	419
QY	421	FNKEADOTGSVVFSGATVNSADFHORNLOTKTPAPLTLSNGFLCIEDHAQLTWNRTQTG	480
DB	420	FNKDSQIGCVVFGATVLSADISQANLQTKTPATLTLSHGLLCTEDRAQLTVNNFTQTG	479

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QY 481 GWSLGNAGAVLSYKNGAGN-----SASNASITLKHIGLNLSSILKSGAEIPLLWVE 532
Db 480 GIVALGNAGVLSVQSHSTTDATQTPPTTTTDDASVTLNHNGLNPSILKDGAEPLLWVE 539
QY 533 PTN-----NSNNYTADTAATFSLSDVKLSLIDDYGNSPYESTDLTHALSSQPMLSISEASD 588
Db 540 PISTQGTNTTYSDDTAASFSLNGATLSLIDEDGNSPYENTDLSRALYAQPMALISEASD 599
QY 589 NQLSDDDMFEGSLNVPYHGWGLTWGAKTQDEPAPASSATIIDPOKANRHRRLTLTLWL 648
Db 600 NQLQSESMDFSKVNPVHYWGGLTWGAKTENPTTTPPATITDPKKANQFHRLLTLWL 659
QY 649 PAGVVPKPKHSPLIANTLWGNMLLATESLKNASLAPSDHPFGWITGGGGLCMVYQDPR 708
Db 660 PAGVVPKPKHSPLIANTLWGNMLLATESLKNASLAPSDHPFGWITGGGGLCMVYQDPR 719
QY 709 ENHPGFHMRSGSYGAGMIAGTQTFSLKFSQTYTKLNERYAKNVSNNYSCQGEMLFSL 768
Db 720 KDHGPFHMRSGSYGAGMITGNTHTFSLRFQSQYTKLNERYAKNVSNNYSCQGEMLFSL 779
QY 769 QEGFLTLKVLGLYSYGDHNCHEFTVTOGENTLSQCTERSOTMGAVFEDLPKPKSGSTHIL 828
Db 780 QEGFLTLKVLGLYSYGDHNCHEFTVTOGENTLSQCTERSOTMGAVFEDLPKPKSGSTHIL 839
QY 829 TAPFALGALGYSSLSHFTEVGAYRPSFSTKPTLINVLVPIGVKGSFNMATQPOAWTVEL 888
Db 840 TAPFALGALGYSSLSHFTEVGAYRPSFSTKPTLINVLVPIGVKGSFNMATQPOAWTVEL 899
QY 889 AYQPVLYRQEPGIATQALLASKGIWFGSGSPSRHMSYKISQQTQPISLWFLFLFYHGFF 948
Db 900 AYQPVLYRQEPGIATQALLASKGIWFGSGSPSRHMSYKISQQTQPISLWFLFLFYHGFF 959
QY 949 SSSTFCNVLNGEIALRF 965
Db 960 SSSTFCNVLNGEIALRF 976

RESULT 3
PM15_CHLPN
ID PM15_CHLPN STANDARD; PRT; 938 AA.
AC Q92883;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE Probable outer membrane protein pmp15 precursor (Polymorphic membrane
protein 15).
DE PMP15 OR CPN0466 OR CP0286.
GN Chlamydia pneumoniae (Chlamydophila pneumoniae).
OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydophila.
OX NCBI_TaxID=83558;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AR39;
RX MEDLINE=99206606; PubMed=10192388;
RA Kalman S., Mitchell W., Marathe R., Lammel C., Fan J., Hyman R.W.,
RA Olinger L., Grimwood J., Davis R.W., Stephens R.S.;
RT "Comparative genomes of Chlamydia pneumoniae and C. trachomatis.";
RL Nat. Genet. 21:385-389(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=AR39;
RX MEDLINE=20150255; PubMed=10684935;
RA Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
RA White O., Hickey E.K., Peterson J., Utterback T., Berry K., Baas S.,
RA Linher M., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,
RA Gwin M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.,
RA Eisen J., Fraser C.M.;
RT "Genome sequences of Chlamydia trachomatis MoPn and Chlamydia
pneumoniae AR39.";
RL Nucleic Acids Res. 28:1397-1406(2000).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=J138;
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RX MEDLINE=20330349; PubMed=10871362;
RA Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K.,
RA Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.;
RT "Comparison of whole genome sequences of Chlamydia pneumoniae J138
from Japan and CWL029 from USA.";
RL Nucleic Acids Res. 28:2311-2314(2000).
CC -1- SUBCELLULAR LOCATION: CELL WALL SURFACE (ELEMENTARY BODIES)
(POTENTIAL).
CC -1- SIMILARITY: BELONGS TO THE PMP OUTER MEMBRANE PROTEIN FAMILY.
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CC EMBL; AE001631; AAD18608.1; -
DR EMBL; AE002190; AAF38143.1; -
DR EXBL; AP002546; BAA98672.1; -
DR TIGR; CP0286; -
DR InterPro; IPR003368; Chlamydia_PMP.
DR InterPro; IPR003357; OMP.
DR Pfam; PF02385; OMP; 1.
DR Pfam; PF02415; DUF145; 1.
KW Outer membrane; Signal; Multigene family; Complete proteome.
FT SIGNAL 17 POTENTIAL.
FT CHAIN 18 938 PROBABLE OUTER MEMBRANE PROTEIN PMP15.
SQ SEQUENCE 938 AA; 102194 MW; A904AAB05B567455 CRC64;

Query Match 22.0%; Score 1120.5; DB 1; Length 938;
Best Local Similarity 30.9%; Pred. No. 7.7e-63;
Matches 308; Conservative 163; Mismatches 418; Indels 109; Gaps 31;

QY 6 FFFLIGNSLGLAREVPSRIFLMPNSVDPDTKESLNSKISLTGDTNLT-----NC 56
Db 12 FTFVLN--EGLQLPLEYITLSPEYQAQP-----VGFTTHNQDLAIVGNHD 59
QY 57 YLDNRYLAILQKTPNEGAATITDYLSPFDQKEGIFAKNLTPESGGGAIGVASPNP 116
Db 60 FILDYKYY-----RSNGALTCKNLL--ISENIGNVFEKKNVCPNSGAI-YAAQNC- 108
QY 117 TVEIRDTIGPVIFENNTCCRPFTSSNPAAVNKIREGGAIIHAQNLVHNHDDVGVGFMKNF 176
Db 109 -----TISK--NQYAFETNLVSDNPTATAGSL--GGALFAINCSTNNLQOGTFVDNL 159
QY 177 SYVRGGAISTANTFVYSENQSCFLFMDNICIQTNTAGKGGAIYAGTSNFSNCCDLFFI 236
Db 160 ALNKGALYETNLSIKDNKGPITIKQNRAL--NSDSLGGGIYSGNSLNEGNSGAIQIT 217
QY 237 NNACCAGGAIFS-PICSLTGNRGNIVFYNNRCFKNVEVASSEADGGAIKVTRLDVTGN 295
Db 218 SNSSGGGIIFTQTTLTSSNKKLIEISENSAFAN--NYGSNFPNGGGGLTTTFTCLNN 275
QY 236 RGRFFSDNITKNYGGAIYAPVTVLDNGPVYFINNIANNKGAIYID-GFSNSK--ISA 352
Db 276 REGVLFNNOQSNGGAIHAKSIIKENGVPYFLNNTATRGALLNLNAGSNGSFLISA 335
QY 353 DRHAIIFNENIVTNVANGTSTSANPPRNATVASSSGEILLGAGSSQNLIIFYDPIEV 412
Db 336 DNGDIIFNN-----TASKHALNPPYRNAIH-STPMNMLQICARGYRVLFYDPIEH 386
QY 413 S-NAGVSVFNKEADQTSVVSFGATVNSADFQHNRLQTKTPAPLTLSNGFLCTEDHAQL 471
Db 387 ELPSSFPILFNFTGHTGTGLVSGEHVQNFTEDEMFFSYLRNTSELRQGVLAVEDGAGL 446
QY 472 TVNRTQGTGGVSLNGAVLSCYKNGAGN-----SASNASITLKHIGLNLSSILKSG 523
Db 447 ACYKFFQRGGTLILGQGAIVTT---AGTIPTSPSTPTVGTSTIFLNHIALDLSILSFQ 502
QY 524 AEIPLLWVEPTNNSNNTADTAATFSLSDVKLSLIDDYGNSPYESTDLTHALSSQPMLSI 583
Db 583 AEIPLLWVEPTNNSNNTADTAATFSLSDVKLSLIDDYGNSPYESTDLTHALSSQPMLSI 583
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QY 641 RTLLTLPAGYVSPKHSRPLIANTLWGNMLLATESLKNSAELTPSD--HPFWGITGG 698
Db 627 RALYANWTPGKYVNFYQGLATPLWQSFHFWFSLRYSNRTGSDIERPLEIQGIA 686
QY 699 LGMMVQDPRENHPGFHMRSSGYS--AGMTAGOTHTFSLKFSQTYTKLNERYAKNNVSSK 756
Db 687 DGLFVHQNSIPGAPGFRIOQSTGYSIQASSETSLHQISLGFQAFQFTRTKEIGSSNNVSAH 746
QY 757 N--YSCQGMFLSLQEGFLTKLVGLYSYGDHCHHIFTYOGENLTSGOTFSRQTMGAVF 814
Db 747 NTVSSLYVELPW-FQFAF-ATSTVLAYGYGDHHLHSLHPSHQE-QAEGTCYSHTLAAIG 803
QY 815 FDLPMKPFSGTHILTAFFLGCALGYSLSHFTVEGVYPRSFSTKTPLINVLVPIGVKGSF 874
Db 804 CSFPWQOKSVLHL--SPFVQAIARSHQTAFAEIGDNPFRKFSQKFEYNTLPLGIGQKW 861
QY 875 MNATORQAWVELAYOPVLYRQEPGIATOLLASKGIWFGSGSPSRHMSYKISQOTQP 934
Db 862 QSRFHVPTEWTELSYQVLYQONPQIGVTLASGGSDILGHNVYRNALGYKVHNOTAL 921
QY 935 LSWLTLHFQYHGYSSTFCNYLNGEIALRF 965
Db 922 FRSLDLFLDYQGSVSSSTSTHHLQAGSTLKF 952

RESULT 5
PM18_CHLPN STANDARD; PRT; 946 AA.
AC Q92880; Q9RB60;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Probable outer membrane protein pmpl8 precursor (Polymorphic membrane
DE protein 18).
GN PM18 OR CPN0471 OR CP0283.
OS Chlamydia pneumoniae (Chlamydophila pneumoniae).
OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydophila.
OX NCBI_TaxID=83558;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CWL029;
RX MEDLINE=99206606; PubMed=10192388;
RA Kalman S., Mitchell W., Marathe R., Lammel C., Fan J., Hyman R.W.,
RA Olinger L., Grimwood J., Davis R.W., Stephens R.S.;
RT "Comparative genomes of Chlamydia pneumoniae and C. trachomatis.";
RL Nat. Genet. 21:383-389(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=AR39;
RX MEDLINE=20150255; PubMed=10684935;
RA Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
RA White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S.,
RA Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,
RA Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.,
RA Eisen J., Fraser C.M.;
RT "Genome sequences of Chlamydia trachomatis MoPn and Chlamydia
RT pneumoniae AR39.";
RL Nucleic Acids Res. 28:1397-1406(2000).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=J138;
RX MEDLINE=20330349; PubMed=10871362;
RA Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K.,
RA Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.;
RT "Comparison of whole genome sequences of Chlamydia pneumoniae J138
RT from Japan and CWL029 from USA.";
RL Nucleic Acids Res. 28:2311-2314(2000).
CC -! SUBCELLULAR LOCATION: CELL WALL SURFACE (ELEMENTARY BODIES)
CC -! POTENTIAL.
CC -! SIMILARITY: BELONGS TO THE PMP OUTER MEMBRANE PROTEIN FAMILY.
CC -----
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CC -----
CC EMBL: AE001631; AAD18610.1; -
CC EMBL: AE002189; AAF38141.1; -
CC EMBL: AF002546; BAA98677.1; -
CC TIGR: CP0283; -
CC -----
CC InterPro: IPR003368; Chlamydia_pmp.
CC Pfam: PF02385; OMP; 1.
CC Outer membrane; Signal; Multigene family; Complete proteome.
CC SIGNAL 16 POTENTIAL.
CC CHAIN 17 946 PROBABLE OUTER MEMBRANE PROTEIN PMP18.
CC CONFLICT 426 426 A -> T (IN REF. 1).
CC CONFLICT 882 882 V -> I (IN REF. 1).
CC SEQUENCE 946 AA; 103611 MW; DCBF6B3D04AC452C CRC64;
Query Match 18.7%; Score 951.5; DB 1; Length 946;
Best Local Similarity 29.1%; Pred. No. 3.3e-52;
Matches 281; Conservative 168; Mismatches 416; Indels 101; Gaps 34;
QY 35 PTYESLSNKISLTGDTNLT-----NCYLDNRLRYLAILQKTPNPGAATITDYL 84
Db 47 PLIDTLTN---MTPYSHRATLFGVRDDTNQDILVDHONSIESWFENSQDGGALSKS-L 102
QY 85 SFEDTOKEGIYFAKNTLTPESGGAIGVYASPNSPVETRTDGTGVFENNTCCRFPTSSNP 144
Db 103 AYTNT-KNQLFLNSFAIKRAGAM-YVNGN---FDISENHGSIIFSGNL-----SFPN 150
QY 145 AA--VVKIREGGAHQAOLYINIHNDVYGVPMKFNFSYVRGGAISTANTFVYSENQSCFLEM 202
Db 151 ASNFADTCTGGAVLCKNVTISKNGTAYFINNKAQSSGGAIAQAAIINIKNDTGPCLFF- 209
QY 203 DNTCIQTNTAG--KGGAIYAGTNSFESNCDLFFINNACCAGAI-FSPICSLTNGRN 259
Db 210 -----NNAAGGTAGGALFANACR-IENNSQPIYFLNNQSLGGLGAIRVHCEILTKNTGS 262
QY 260 IVFNRCFKNVETASSEASDGAIAKVTRLDVTGNRGRIFFDSDNTTKNGKIYAPVVT 319
Db 263 VIFNNN-FAMEADISANHSSGGAICYIS-CSIKDNPFGIAFDNNTAARDGGAICTQSLT 319
QY 320 LVDNGPTYFINNIANNKGAIIYIDGTSNSKISADRAHAIIFENIVTNVNTANGTSTANP 379
Db 320 IQDSGPVYFTNN-QGTWGGAILRLQDQACTLFADQGDIIFFNNRHFKDTFSN-HVSVNC 376
QY 380 PRNATVASSSGEILLGSSONLIFYDPI-----EVSNAGVSYSNKEADQTSVVFSG 435
Db 377 TRNVSLTVGASQG-----HSATFYDPILOQRTYIONS--IQKFNPNPEHLGTLFSS 425
QY 436 A-----TVNSADR--HORNLOTKTPAPLTLSNGFLCEDHAOLTVAAREFTQGVVSLNG 488
Db 426 AYTPTDSTSDDFISFRN-----HIGLYNGTLEADRAEWKVKYKDFQGGTLRGSR 478
QY 489 AVLSCYKNGAGNSASNASITLKHIGLNSLSKASGEIPLLVWETPNNSNNTYADTAATF 548
Db 479 AVFTTDEQSSSSVGVSVININLAINLPSIL-GNRVAPKLWIRPTGSSAPYSEDNNPII 537
QY 549 SLSDVKLSLIDDYGNSPYESTDLTHALSQPMLSISEASDNQJRSDDMPFSGLN-VPHYG 607
Db 538 NLSG-PLSLDDENLDPYDTADLAQPIAEVPLLYLLDVTAKHINTDNFYPEGLNTTQHYG 596
QY 608 WQGLTWGAKTQDPEPASSATITDPKANRPHRTLLLTWLPAGYVSPKHSRPLIANTL 667
Db 597 YQGVWSPYIETITTTSDTSS-----EDTVNTLHRQLYGDWTPGTGYKVPENKDIASAF 651
QY 668 W---GNMLLATESLKNSAELTPSDHPFWGITGGGLGMVYQDPRENHPGFHMRSSGYSAG 724
Db 652 WQSFHNLFTALRYQTQGGIAPT-----ASGEATRLFVHNSNNDKAGFHMERTGYSLG 705
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QY 945 HGFYSSFTFCNLYNGEIALRF 965
DB 1014 QAEVATSTVSHVAGGALVF 1034

RESULT 7
PMPF_CHLMO STANDARD; PRT; 1025 AA.
AC Q9PL46;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, last sequence update)
DE Probable outer membrane protein pmf precursor (Polymorphic membrane
DE protein F).
GN PMPF OR TC0262.
OS Chlamydia muridarum.
OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
ON NCBI_TaxID=83560;
RX SEQUENCE FROM N.A.
RC STRAIN=MoPn / Nigg.
RA MEDLINE=20150255; PubMed=10684935;
RA Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
RA White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S.,
RA Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,
RA Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.,
RA Eisen J., Fraser C.M.;
RA "Genome sequences of Chlamydia trachomatis MoPn and Chlamydia
RT pneumoniae AR39.";
RL Nucleic Acids Res. 28:1397-1406(2000).
CC -!- SUBCELLULAR LOCATION: CELL WALL SURFACE (ELEMENTARY BODIES)
CC (POTENTIAL).
CC -!- SIMILARITY: BELONGS TO THE PMP OUTER MEMBRANE PROTEIN FAMILY.
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CC
CC ENBL; AE002293; AAF39131.1; .
DR TIGR: TC0262;
DR InterPro; IPR003368; Chlamydia_PMP.
DR InterPro; IPR003357; OMP.
DR Pfam; PF02385; OMP; 1.
DR Pfam; PF02415; DUF145; 1.
KW Outer membrane; Signal; Multigene family; Complete proteome.
FT SIGNAL 1 20 POTENTIAL.
FT CHAIN 21 1025 PROBABLE OUTER MEMBRANE PROTEIN PMPF.
SQ SEQUENCE 1025 AA; 111458 MW; EA472E07818B9FF2 CRC64;

Query Match 15.6%; Score 793; DB 1; Length 1025;
Best Local Similarity 27.0%; Pred. No. 3.4e-42;
Matches 269; Conservative 158; Mismatches 419; Indels 152; Gaps 35;

QY 68 LQKTPNEGAATITDYLSFFDTQKEGYFAKNLTPESGGAIGYASPNPTVEIRDITGPV 127
DB 80 LSTTSSGAFY-ESMTSFTAIADNADLFFCCNNYCTHOGG--GGAINATGLISFKNNQNIL 135
QY 128 IFENNTCCRPFTSSNPAVKNIREGAIHAQNLNHNHDDVGVFMKNFVSVRGGAISTA 187
DB 136 FYNNTIGTQPTGVALRTERNR---GGALYGSSELINNHNS-LNFINNTSGDMGAVSTI 191
QY 188 NTFVVENQSCFLFMDNICIO--TNT----AGKGAIYAGTSSNFESNCCDLFFINACC 241
DB 192 QNLVIKNTSGIVAFENHHTDHIPTATILARGAVCCQACAEISHNTGVPVFNNSYGG 251
QY 242 AGGAIFS-PICSLTGNRGNIVFYNNRCFKNVETASSASDGAIKVTRLDVTGNRGRIF 300
DB 252 YGGAISTGGOCIFRDKDKLIFINNSALGWHNT--SAQGNNAVISAGEFGLLNKGPY 309
```


RA Christiansen G., Boesen T., Hjerno K., Daugaard L., Mygind P.,
 RT Madsen A.S., Knudsen K., Falk E., Birkelund S.;
 RT "Molecular biology of Chlamydia pneumoniae surface proteins and their
 role in immunopathogenicity";
 RL Am. Heart J. 138:5491-5495(1999).
 CC -!- SUBCELLULAR LOCATION: CELL WALL SURFACE (ELEMENTARY BODIES)
 CC (POTENTIAL).
 CC -!- SIMILARITY: BELONGS TO THE PMP OUTER MEMBRANE PROTEIN FAMILY.
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 CC EMBL; AE001627; AAD18589.1; -;
 CC EMBL; AE002193; AAF38165.1; -;
 CC EMBL; AF002546; BAA98653.1; -;
 CC EMBL; AJ133034; CAB37067.1; -;
 CC PHCJ-2DPAGE; Q92898; -;
 CC TIGR; CF0308; -;
 CC InterPro; IPR003368; Chlamydia_PMP.
 CC InterPro; IPR003357; OMP.
 CC Pfam; PF02385; OMP; 1.
 CC Pfam; PF02415; DUF145; 2.
 KW Outer membrane; Signal; Multigene family; Complete proteome.
 FT SIGNAL 1 23
 FT CHAIN 24 936 PROBABLE OUTER MEMBRANE PROTEIN PMP7.
 FT CONFLICT 658 666 PTHGRFRI -> EDNIRYRN (IN REF. 4).
 FT CONFLICT 822 822 Y -> H (IN REF. 1 AND 4).
 SQ SEQUENCE 936 AA; 100105 MW; 3981DB3C950AF95A CRC64;

Query Match 12.7%; Score 644; DB 1; Length 936;
 Best Local Similarity 27.0%; Pred. No. 6.9e-33;
 Matches 262; Conservative 146; Mismatches 392; Indels 172; Gaps 44;

QY 75 GAAVTITDVLSPFDQKEGIYFAKNTPESSGGAIGV-----ASPNSPVVEIR 121
 DB 54 GTTYSLLSDVSFONAGALGPIASGCFLEAGDGLTFQGNHAKLFAFINAGSAGTVAST 113
 QY 122 DTIGPVIFENN-----TCCRPFTSSNPAAVNKIREGGAIHAQNLINHNHDVVGFMK 174
 DB 114 SAADKKNLLEFNDSRLSIISCPSSLSPGQALKSV-----GNLSLTGNSQII-FTQ 164
 QY 175 NFSYVGGGAISTANTFVWSENQCFLEPMONICIQTNVAGKGGAIYA-GTNSPESFNCDL 233
 DB 165 NFSSDNGGVINTKN-FLLSGTSQFASFERN--QAFTGKGGVYVYATGTTIENSPIVS 220
 QY 234 FFFNNACAGGAIFS-PICSLTGNRGNIVFYNNRCFKNVTASSEASDGGAIKVT--R 289
 DB 221 FSNLAKSGGALYSTDNKSIDTN-FQVIFDGNSEAAQ-----AQGGAICTTDTKT 273
 QY 290 LDVTGNRGRIFSDNTKNYGGAIYAPVTVLDVNGTPTFYFINNANK-----GGAIIYIDG 344
 DB 274 VTUTGNK-NLSEFTNNTALTYGGAISGLKVSISAGGPTLFQSNISGSSAGOGGGAINIAS 332
 QY 345 TSNKSKISADRHAIFFENIVTNVNTANGTSTANPPRRNAITVASSSGEILLGAGSQNL 404
 DB 333 AGEALASATSGDITFNQNVN-----GSTST-----RNAINTIDKAVTSIRAATGQSI 382
 QY 405 IFYDPIEVSNAGVS-----FNKEADOTGSVFSGATVNSAD-FHQRLQTKP 453
 DB 383 YFDPI--TNPGGFASTDTLNLNLDANSEIEVGGAIVFSGEKLSTPEKAIAANVTSTIR 440
 QY 454 APLTSLNGFLICIEDHAQLTVNRTQTGGVYSLGNAGVLSCKYKAGNASNASITLKHIG 513
 DB 441 QPAVLARGDLVLRGVTVTFKDLTQSPGSRILMDG-----GTLSAKEANLSNLGA 492
 QY 514 LNUSSILKSGAEIPLWVEPTNNNNYTAATAATFSLSDVKLSLIDDYNGSPYESTDLTH 573
 DB 493 VNLSSL-----DGTNKAALKTEAADKNISLSGT-IALIDTEG-SFYENHNILKS 538

QY 574 ALGSOQMLISSEASDN-QLRSDDDMFSGLNVP--HYGWOGLWTGWAKTQDPEPASSATI 630
 DB 539 A-STYPLLELTAGAGNTITLGAISLTITLQEPETHGYQGNWOLSWAN-----ATSSKI 591
 QY 631 TDPQKANRFRHTLLTWLPAGYVPSPKHRSPLIANTLWGNMLLATESLKNSAELTPSDHP 690
 DB 592 GS-----INWTRGTIPIPSPERKSNLPLNSLWGN-FIDIRSIQLIETKSSGEP 638
 QY 691 F-----NGITGGGLGMVYQDPRENHPGFRMRSSGYSGAGMIAGQTHFSLKFSQTYTKLNE 746
 DB 639 FERELW---LSGIANEFYRDSMPTRHGFRHISGGYALGITATPAEDQLTFA--FCQLFA 693
 QY 747 RYAKNNVSSKN-----YSCQGEMLFSLQEGFL-----LTKLVGL----- 780
 DB 694 R-DRNHTGKHGDDTYGASLYFHHTGLFDI-ANFLMGKATRAPVULSEISQIIPISFDA 751
 QY 781 ---YSYGDHNCHEFTYTGENTLSQGTFRSOTMGGAFFDLPMPFGSTHIL--TAPFLGA 835
 DB 752 KFSYLHTDNHMKTYT--DNSIIKGSWRNDAFCADLGASLPF-VISVPYLLKEVEPEVKV 808
 QY 836 LGIYSSLSHTEVGCAYPRSESTKTPLINLVPIGVKGSFMNATQRPQAWTVLAYQDVL- 894
 DB 809 QYIYAHQQDFYRYAEGRAFNF-KSELINVEIPIGVT---FERDSKSEKGYDITLMLYILD 864
 QY 895 -YRQEPGIATQLLASKGIWFGSGSPSRHAMSYSKISQOTQPLSWLTLHFQYHGFYSSTF 953
 DB 865 AYRNPKCQTSLIASDANWAGTNLARQGSFVRAAHFQVNHFMHFEFGQF-AFEVRSSS 923
 QY 954 CNYLNGEIALRF 965
 DB 924 RNY-NTNLGSKF 934

RESULT 10
 PMPG_CHLMU
 ID PMPG_CHLMU STANDARD; PRT; 987 AA.
 AC O9PL45;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Probable outer membrane protein pmpG precursor (Polymorphic membrane
 protein G).
 GN PMPG OR TC0263.
 OS Chlamydia muridarum.
 OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
 OX NCBI_TaxID=83560;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MoPn / Nig9;
 RX MEDLINE=20150255; PubMed=10684935;
 RA Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
 RA Linher K., Hickey E.K., Peterson J., Otterback T., Berry K., Bass S.,
 RA Gwin M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.,
 RA Eisen J., Fraser C.M.;
 RT "Genome sequences of Chlamydia trachomatis MoPn and Chlamydia
 pneumoniae AR39";
 RL Nucleic Acids Res. 28:1397-1406(2000).
 CC -!- SUBCELLULAR LOCATION: CELL WALL SURFACE (ELEMENTARY BODIES)
 CC (POTENTIAL).
 CC -!- SIMILARITY: BELONGS TO THE PMP OUTER MEMBRANE PROTEIN FAMILY.
 CC
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 CC
 CC EMBL; AE002293; AAF39132.1; -;
 DR TIGR; TC0263; -;

DR EMBL: AE001627; RAD18590.1; -;
DR EMBL: AE002193; AAF38164.1; -;
DR EMBL: AP002546; BAA98654.1; -;
DR PHCI-2DPAGE; Q9Z393; -;
DR TIGR: CP0307; -;
DR InterPro; IPR003368; Chlamydia_PMP.
DR InterPro; IPR003357; OMP.
DR Pfam; PF02385; OMP; 1.
DR Pfam; PF02415; DUF145; 2.
KW Outer membrane; Signal; Multigene family; Complete proteome.
FT SIGNAL 1 26
FT CHAIN 27 930 PROBABLE OUTER MEMBRANE PROTEIN PMP8.
FT CONFLICT 177 177 T -> A (IN REF. 3 AND 4).
SQ SEQUENCE 930 AA; 97669 MW; 46A9B5E3BB913C4C CRC64;

Query Match 12.1%; Score 617; DB 1; Length 930;
Best Local Similarity 27.0%; Pred. No. 3.4e-31;
Matches 251; Conservative 140; Mismatches 374; Indels 164; Gaps 40;

QY 47 TGDTHNLTCYLDNLRILAILQKTPNEGAAYT---ITDYLSPFDFTQKEGIYFAKLTPE 103
DB 50 TADA-NGTVNLVSGNVI-----NDAGKGTALTGCCFTETGDLFTGKGYSEFN-TVD 102
QY 104 SGAGIYASPNPTVEIRDT-----TGPVIFENNTCCRPFTSSNPNAVNKIRREGGAHQA 159
DB 103 AGSNAGAAASTTADKALTFTGFSNLSTFIAAPGTTVASGKSTLSSAGALNLTGNTILFSQ 162
QY 160 NLYININHVDVGMKFNFSYVGRGAISTANTFVVSQSCFLFMDNICIOTNTAGK-GGAI 218
DB 163 NVSEANNN-----GGAITP-KTLSISGNTS-----SITFTSNSAKLGGLAI 203
QY 219 YAGTNSFESNCDLFFINN-ACCAGGAI-FSPICSLTGNRGNIVFYNNRCFKNVETASS 276
DB 204 YSSAAASISGNTQGLVFMNKGCTGGALGFEASSITQN-SLSPFSGN-----TATD 255
QY 277 EASDGAIVK-----TTRLDVTGNRGRIFPSDNITKNYGGAIYAPVVTLVNDNGPTVIN 331
DB 256 AAGKGAIYCEKTEPTTITISGNKS-LTFAENSSVTQGAICAHGLDLSAAGPTLFSNN 314
QY 332 IANN-----KGGAIYIDGTSNKISADRHAIIFENIVTNVNTANGSTSANPRRAIV 387
DB 315 RCNTAAGKGAIATADSGLSANQGDITLGNLT-----TSTAPSTRNAYIL 366
QY 388 ASSSGEILLGAGSSQNLIFDIPTVSNAGVS-----VSFNKEADQTSVVFSGATVNS 440
DB 367 GSSAKITNLRAGQGSIIYFDPIASNTTGCASDVLTIQPDNSPLDYSGTIVFSGEKL-S 425
QY 441 ADPHQR--NLQKTPAPLPLNSGFLCIEDHAQLTVNRFTQTGGVVSGLNGAVLSCYKNGA 498
DB 426 ADEAKAADNFTSILKQPLALASGTLAKGNVELDVNGFTQTEGSTLL-----MQPGT 477
QY 499 GNSASNASITLKHIGLNLSSILKSGAEIPLLWVEPTNNSNNTADTAATFSLSDVKLSLI 558
DB 478 KUKADTEALSLKLVVDLSAL-----EGNKSVSIEFAGANKTITLTS-PLVPQ 524
QY 559 DDYGNSPYESTDLTHALSSQPLMSISEASDNLRRSDMDPFGNLV-----PHYGWOGL 611
DB 525 DSSGNF-YESHTINQAF-TQPLVVFTAA-----AASDIYIDALLTSPVQTPPEHYGQGH 578
QY 612 WTGWAKTQDPPASATITDPOKANRFRHTLLTWLPAGYVPSPKRHSPLIANTLWGNM 671
DB 579 WEATWA---DTSTAKSGT-----MTWVTGYNPNPERRASVVPDLSLWASF 620
QY 672 LLATESLKNSAELTPSDHPFW---GITGGGLGMVMYQDPRENHGPMPHMBSSGYSAGMIAG 728
DB 621 ---TDTRTQQIMTSQANSIYQORGLWASGTANFFHKDKSGTNGQAFRHKSYIVVGSAG 677
QY 729 --QTHFTSLKFSQTYTKLNRVAKNNVSKNYSQ-----GEMFLSLQ 769
DB 678 DSENIFFSAVFCOLFCKDKDLFIVEN-TSHNVLASLYLQHRAFLGGLPMPSPGSIIDMLK 736
QY 770 EGFLLTKVLGVSYGDNCHHEFT-----QGENLTSQGTFRSQTMGGAVFFDLPMK-PFG 823

DB 737 DIPLILNAQLSYSTKNDMDTRTYSYPEAQGSWTNNSGALE---LGGSLALYLPKEAPFF 793
QY 824 SHHILTAPELGAIGIYSSLSHTEVCAYPRSFSTKPLINLVLPICVKGSFNNATQRPQA 883
DB 794 QGYF---PFLKFOAVYSRQONFKESGAERAFD-DGDLVNCSPVIGIRLEKISEDEK-NN 848
QY 884 WTVELAYQPVLYRQEPGIATQIASKGIW 912
DB 849 FEISLAYIGDVYKRNPRSRSTSLMVSASW 877

RESULT 12
PMP11_CHLPN
ID PMP11_CHLPN STANDARD; PRT; 928 AA.
AC 086164; O9K299;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE Probable outer membrane protein pmp11 precursor (Polymorphic membrane protein 11) (Outer membrane protein 4).
GN PMP11 OR OMP4 OR CPN0449 OR CP0302
OS Chlamydia pneumoniae (Chlamydia pneumoniae).
OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
NCBI_TaxID=83558;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CWL029/VR-1310;
RX MEDLINE=99081766; PubMed=9864239;
RA Knudsen K., Madsen A.S., Mygind P., Christiansen G., Birkelund S.;
RT "Identification of two novel genes encoding 97- to 99-kilodalton outer membrane proteins of Chlamydia pneumoniae";
RL Infect. Immun. 67:375-383(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=VR1310;
RX MEDLINE=20007384; PubMed=10539856;
RA Christiansen G., Boesen T., Hjerno K., Dagaard L., Mygind P.,
RA Madsen A.S., Knudsen K., Falk E., Birkelund S.;
RT "Molecular biology of Chlamydia pneumoniae surface proteins and their role in immunopathogenicity";
RL Am. Heart J. 138:S491-S495(1999).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=CWL029;
RX MEDLINE=99206606; PubMed=10192388;
RA Kalman S., Mitchell W., Marathe R., Lammel C., Fan J., Hyman R.W.,
RA Olinger L., Grimwood J., Davis R.W., Stephens R.S.;
RT "Comparative genomes of Chlamydia pneumoniae and C. trachomatis";
RL Nat. Genet. 21:385-389(1999).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=AR39;
RX MEDLINE=20150255; PubMed=10684935;
RA Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
RA White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S.,
RA Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,
RA Gwin M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.,
RA Eisen J., Fraser C.M.;
RT "Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39";
RL Nucleic Acids Res. 28:1397-1406(2000).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=J138;
RX MEDLINE=20330349; PubMed=10871362;
RA Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K.,
RA Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.;
RT "Comparison of whole genome sequences of Chlamydia pneumoniae J138 from Japan and CWL029 from USA";
RL Nucleic Acids Res. 28:2311-2314(2000).
CC -!- SUBCELLULAR LOCATION: CELL WALL SURFACE (ELEMENTARY BODIES) (POTENTIAL).
CC -!- SIMILARITY: BELONGS TO THE PMP OUTER MEMBRANE PROTEIN FAMILY.

DR Pfam: PF02385; OMP; 1.
DR Pfam: PF02415; DUF145; 2.
KW Outer membrane; Signal; Multigene family.
FT SIGNAL 1 25 POTENTIAL.
FT CHAIN 26 928 PROBABLE OUTER MEMBRANE PROTEIN PMP10.
SQ SEQUENCE 928 AA; 97229 MW; 0590D5206A1DD0E1 CRC64;

Query Match 11.5%; Score 586.5; DB 1; Length 928;
Best Local Similarity 25.6%; Pred. No. 2.8e-29;
Matches 264; Conservative 143; Mismatches 377; Indels 249; Gaps 48;

QY 1 MKKAFVFLIGNSL-----SLAREV-PSRIF-----LMPNSVDPDTKESLS 41
DQ 1 MKSQSWLVLSLACFTSCSTVFAATAENIGSDSFDGSTNTGTVPKNTTGTIDYTLT 60
QY 42 NKISL--TGDTHNLT-NCVLDNLR-----YILAIQ-KTPNEGAATIT----- 81
DQ 61 GDTLQNLGDSAAALTKGCFSDTESLSFAGKYSLSFLNKSASGAALSVTDDKNLSLT 120
QY 82 --DYLSTFDQKQGYFAKNLTPESGGAIGYASPSPTVEIRDTPGVIFENNTCCRPPT 139
DQ 121 GFSLTLFLAAPSVI-----TTPSGKGAVKCGDLT-----FDNNGTILFKQDYC----- 165
QY 140 SSNPNAVNKIREGGAHAQNIYINHHVDVGFMKNFYSVVRGGAISTANTFVYSENQSCF 199
DQ 166 -----EENGGAISTKNSLNSTGSISEGNKS----- 193
QY 200 LFMNDCIOTNAGKGAIGYAGTSNSFSNCCDLFFINN-ACCAGGAIFSP-ICSITGNR 257
DQ 194 -----SATKKGGAICATGVDITNTNAPTFLSNIAEAGAISTNCITGNT 244
QY 258 GNIVYNNRCFNKVFETASSEADGGAIKVTRLDVTGNRGRIFDSDITKNGGAIYAPV 317
DQ 245 -SLVSEN-----SVTATAGGAGALSGDADVTISNGQS-VTFSGNQAANGAIYAKK 295
QY 318 VTLVD--NCPYFINNIAN-----NKGAIYIDGTSNKSISADRHAIIFENIVTNTNAN 371
DQ 296 LTLASGGGGISFNINVOGTTAGNGAISILAAEGECSLSAAGDITFNGNAI----- 348
QY 372 GTSTANPRRAITVAASSGELLGAGSSONLIYDPIEVSNAQS-----VSFNK----- 423
DQ 349 -VATTPQTKRNSIDIGSTAKITNLRASGHSIFDYDPTANTADSTDTLNLRADAGN 407
QY 424 EADQTSVVFSGATVNS-----ADPHRNLOTKTPAPLTLSNGFLICIEDHAOLTVNRFTQ 478
DQ 408 STDYSGSVFSGEKLSEDAKVAD-----NLSTLQKQVTLTLAGNLVLRKRGVTLDTKGFTQ 463
QY 479 T-GGVVSLGNGAVLSCYKNGAGNSASNAISITLKHGLNLSSILKSGAEIPLLWVEPTNNS 537
DQ 464 TAGSSVIMDAGTTL-----KASTEVTITGLSIPVDS-LGEGKKYVI----- 504
QY 538 NNYTADTAATFSLSDVKLS-----LIDDYGNSPYESTDL--THALSSQPMLSISEASDNOL 591
DQ 505 -----AASASKNVALSGPILLDNQNA-YENHDLGKTQDFEVQLSALGTATITDV 556
QY 592 RSDMDFGSLNVP-----HYGQGLWTGWAKTQDPEPASSATITDPQKANRHFRTLL 645
DQ 557 PA-----VPTVATPHYQGTGWGTWVDDTASTPKT-----KTAFL 593
QY 646 TWLPAGYVSPKPHRSPLANTLWGN--LLATES-LKNSAELTPSDHPWGTGGGLGNM 702
DQ 594 ANVTNGYLPNPRQGLPVNSLWGSFSDIQATQGVIERALSALTCLSDRGFW-----AAGVANF 650
QY 703 VYQDPRENHPGHRSSGYSGAMIAQOT---HTFSLKFSQTVTKLNERVAKNVSNNKYS 759
DQ 651 LDKDKKGERKRYHSGGYAIG-RAQTCSENLISFAFCQLFGS-----DKDFLAKNHT 704
QY 760 CGEMLFSLQE-----GFLLTKLVG-----LYSYGDHNRHFYT-QGEN 797
DQ 705 DTYAGAFYIQTHTGCSGFGICLLDKLPGWSHKLPLVLEQLAYSHVSNLTKYTAPEV 764
QY 798 LTSQTFRSQTMGGAFFDLP--MKPFGSTHLLTAPFLGALGIYSLSHFTVGVAYPRSF 855

DQ 765 KGSWGNNAFNMMLGASSHSYPEYLHCFTD----YAPYIKLNLTYIRQDSFSEKTEGRSF 820
QY 856 STKTPPLINVLPIGVK-GSFMNATQRPQAWTVELAQPVLYRQEPGIAQTOLLASKGIWFG 914
DQ 821 DDSN-LFNLSLPIGVKFEKFSQDND--FSYDLTSLSVPLDRNDPKCTTALVISGASWET 877
QY 915 SGSPSRSRHMSYK 927
DQ 878 YANNLARQALQVR 890

RESULT 15
PM19_CHLPN
ID PM19_CHLPN STANDARD; PRT; 947 AA.
AC Q92813; O9JSE2;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Probable outer membrane protein pmp19 precursor (Polymorphic membrane protein 19).
GN PMP19 OR CPN0539 OR CP0213.
OS Chlamydia pneumoniae (Chlamydia pneumoniae).
OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydiales.
OX NCBI_TaxID=83558;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CPN029;
RX MEDLINE=99206606; PubMed=10192388;
RA Kalman S., Mitchell W., Marathe R., Lammel C., Fan J., Hyman R.W., Olinger L., Grimwood J., Davis R.W., Stephens R.S.;
RT "Comparative genomes of Chlamydia pneumoniae and C. trachomatis."; Nat. Genet. 21:385-389(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=AR39;
RX MEDLINE=20150255; PubMed=10684935;
RA Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F., White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S., Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R., Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L., Eisen J., Fraser C.M.;
RT "Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39."; Nucleic Acids Res. 28:1397-1406(2000).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=J138;
RX MEDLINE=20330349; PubMed=10871362;
RA Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K., Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.;
RT "Comparison of whole genome sequences of Chlamydia pneumoniae J138 from Japan and CML029 from USA."; Nucleic Acids Res. 28:2311-2314(2000).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=J138;
RX MEDLINE=20298986; PubMed=10839753;
RA Shirai M., Hirakawa H., Ouchi K., Tabuchi M., Kishi F., Kimoto M., Tateuchi H., Nishida J., Shibata K., Fujinaga R., Yoneda H., Matsushima H., Tanaka C., Furukawa S., Miura K., Nakazawa A., Ishii K., Shiba T., Hattori M., Kuhara S., Nakazawa T.;
RT "Comparison of outer membrane protein genes omp and pmp in the whole genome sequences of Chlamydia pneumoniae isolates from Japan and the United States."; J. Infect. Dis. 181 Suppl 3:S524-S527(2000).
CC -!- SUBCELLULAR LOCATION: CELL WALL SURFACE (ELEMENTARY BODIES) (POTENTIAL).
CC -!- SIMILARITY: BELONGS TO THE PMP OUTER MEMBRANE PROTEIN FAMILY.
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	EMBL; AE001638; AAD18679.1; -;	
DR	EMBL; AE002181; BAF38083.1; -;	
DR	EMBL; AP002547; BAA98745.1; -;	
DR	HSSP; Q90121; IKPT.	
DR	TIGR; CP0213; -;	
DR	InterPro; IPR003368; Chlamydia_pmp.	
DR	InterPro; IPR003357; OMP.	
DR	Pfam; PF02385; OMP; 1.	
DR	Pfam; PF02415; DUF145; 1.	
KW	Outer membrane; Signal; Multigene family; Complete proteome.	
FT	SIGNAL	1 19
FT	CHAIN	20 947
FT	CONFLICT	453 453
FT	SEQUENCE	947 AA; 103642 MW; 20CE1DEEE1606DF CRC64; E -> D (IN REF. 3).

Query Match	11.5%	Score 586;	DB 1;	Length 947;
Best Local Similarity	25.2%	Pred. No. 3.1e-29;		
Matches 250;	Conservative 173;	Mismatches 390;	Indels 178;	Gaps 47;

[illegible]

Db	662	NNYLNNSVPIQOH---LCVFGGVPVQIMEQNPQKSNLLVQAHGNVG--ARIPFSN 717
Qy	735	LKFSQTYTKLNERAKNNVSKNYSCOGEMLF---SIQEGFLTKLVGLYSYGDHN---C 788
Db	718	TILSAALTQLFSSSQQSNVADKSHA---QILIGTVSLNKSQWALSLSRSSFSYTEDSQVMK 774
Qy	789	HHFTYQGNLTISQGTFRSQWTGGAFFEDLPKMPFGSTHILTAFLGALGIYSSL--SHFT 846
Db	775	HVFPYKG---TSRGSWRNYGWSGVGMSYAY-PKGRYLKMTPEFVDLQ--YTKLVQNPVF 828
Qy	847	EVGAYPRFSFTKTPLIINVLPIGVKGSFMNATORPQAW-TVELAYQPVLYRQEPGIATOL 905
Db	829	ETGVDYPRFSS-SEMTNLSLPIGIALEMRIIGRSSSLFLQVYSYTKDLRVNPQSSASL 887
Qy	906	LASKGIWFGSGSPSSRHAMS-----YKI 928
Db	888	VLNHYTWDIOCVPLGKKEALNTLNSTIKKYI 918

Search completed: February 4, 2003, 20:55:58
Job time : 44 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 4, 2003, 20:55:07 ; Search time 53 Seconds
(without alignments)
1750.372 Million cell updates/sec

Title: US-09-677-752-2
Perfect score: 5086
Sequence: 1 MKKAFFFFLIGNSLGLARE.....GFYSSTFCNYLNGEIALRF 965

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues
Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_73:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4989.5	98.1	964	E71460	probable outer mem
2	3648.5	71.7	976	F81722	polymorphic membra
3	1120.5	22.0	938	F86548	polymorphic outer
4	1120.5	22.0	938	H72074	polymorphic membra
5	1060.5	20.9	952	D81593	polymorphic membra
6	1052	20.7	934	A72075	polymorphic outer
7	1046	20.6	934	G86548	polymorphic outer
8	951.5	18.7	946	C80549	polymorphic outer
9	951.5	18.7	946	D81594	polymorphic membra
10	948.5	18.6	946	C72075	polymorphic outer
11	866.5	17.0	1034	F71460	probable outer mem
12	793	15.6	1025	G81722	polymorphic membra
13	655.5	12.9	1013	G71460	probable outer mem
14	645	12.7	936	C72078	polymorphic outer
15	644	12.7	936	C86546	polymorphic outer
16	644	12.7	936	B81591	polymorphic membra
17	620.5	12.2	987	H81722	polymorphic outer
18	620	12.2	930	D86546	polymorphic outer
19	620	12.2	930	A81591	polymorphic membra
20	617	12.1	930	D72078	polymorphic outer
21	597	11.7	928	H86546	polymorphic outer
22	597	11.7	928	D72077	polymorphic outer
23	597	11.7	949	F81591	polymorphic membra
24	595	11.7	1016	D71460	probable outer mem
25	587	11.5	947	G86557	polymorphic membra
26	586.5	11.5	928	G86546	polymorphic outer
27	586.5	11.5	928	G81591	polymorphic membra
28	586	11.5	947	D72067	polymorphic membra
29	585.5	11.5	928	E86546	polymorphic outer

30	585.5	11.5	928	2	B72077	polymorphic membra
31	583	11.5	978	2	G72076	polymorphic outer
32	583	11.5	978	2	B81593	polymorphic membra
33	583	11.5	978	2	C86547	polymorphic outer
34	575	11.3	973	2	B86547	polymorphic outer
35	575	11.3	973	2	F72076	polymorphic outer
36	575	11.3	995	2	C81593	polymorphic membra
37	570.5	11.2	922	2	B72131	polymorphic outer
38	570.5	11.2	922	2	E86491	polymorphic outer
39	569.5	11.2	922	2	F81539	polymorphic membra
40	567	11.1	1276	2	B86546	polymorphic outer
41	567	11.1	1276	2	C81591	polymorphic membra
42	564	11.1	983	2	A81723	polymorphic membra
43	562	11.0	1407	2	B72078	polymorphic outer
44	546.5	10.7	986	2	B81675	polymorphic membra
45	530.5	10.4	772	2	H86492	Pmp_3 [imported] -

ALIGNMENTS

RESULT 1

E71460

probable outer membrane protein E - Chlamydia trachomatis (serotype D, strain UW3/Cx)
C:Species: Chlamydia trachomatis

C:Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 08-Oct-1999

C:Accession: E71460

R:Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitche

Science 282, 754-759, 1998

A:Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia t

A:Reference number: A71570; MUID:99000809; PMID:9784136

A:Accession: E71460

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-964 <ARN>

A:Cross-references: GB:AE001360; GB:AE001273; NID:g3329342; PIDN:AAC68467.1; PID:g332

A:Experimental source: serotype D, strain UW-3/Cx

C:Genetics:

A:Gene: pmpE

Query Match 98.1%; Score 4989.5; DB 2; Length 964;
Best Local Similarity 98.3%; Pred. No. 3.8e-298;
Matches 949; Conservative 7; Mismatches 8; Indels 1; Gaps 1;

QY	1	MKKAFPPFLIGNSLGLAREVPSRIFLMPNSVDPDPKESLSNKISLTGDTHTNLTNCYLDN	60
Db	1	MKKAFPPFLIGNSLGLAREVPSRIFLMPNSVDPDPKESLSNKISLTGDTHTNLTNCYLDN	60
QY	61	LRYLALQKTPNEGAATITDYLSPFDQKQEGYFAKNLTPESSGGAIGYASPSPTVEI	120
Db	61	LRYLALQKTPNEGAATITDYLSPFDQKQEGYFAKNLTPESSGGAIGYASPSPTVEI	120
QY	121	RDITGPVIFENNTCCRPFTSSNPNAAVNKIREGGAIHAQNLINHHNDVVGVFMKNFSYVR	180
Db	121	RDITGPVIFENNTCCRPFTSSNPNAAVNKIREGGAIHAQNLINHHNDVVGVFMKNFSYVQ	179
QY	181	GGAISTANTVSVENSCFLFMDNICIQTNCTAGKGAIACTNSPESNCDLFFINNAC	240
Db	180	GGAISTANTVSVENSCFLFMDNICIQTNCTAGKGAIACTNSPESNCDLFFINNAC	239
QY	241	CAGGAIFSPICSLTGNRGNITVFNRCFKNVETASSDGGAIKVTTRLDVDTGNRGRIF	300
Db	240	CAGGAIFSPICSLTGNRGNITVFNRCFKNVETASSDGGAIKVTTRLDVDTGNRGRIF	299
QY	301	FSDNITKNYGGAIYAPVVTLLVDNGPTYFINNIANNKGAIYIDGTSNSKISADRHAIFN	360
Db	300	FSDNITKNYGGAIYAPVVTLLVDNGPTYFINNIANNKGAIYIDGTSNSKISADRHAIFN	359
QY	361	ENIVTNVTNANGSTSTANPPRRNAITVASSSGEILLGAGSSQNLIFFDPIEVSNAVSVS	420
Db	360	ENIVTNVTNANGSTSTANPPRRNAITVASSSGEILLGAGSSQNLIFFDPIEVSNAVSVS	419
QY	421	FNKEADTGSVPSGATVNSADFHQNLQTKTPAPLTLSNGFLCIEDHAQLTWNRRFTQTG	480

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Db 420 FNKEADQTSVYFSGATVNSADFHORNLOTKTPAPLTLNSGFLCIEDHAQLTVNRFTQG 479
QY 481 GVVSLGNGAVLSYKNGAGNSASNSITLKHIGLNLSSILKSGAEPLLWVEPTNNSNY 540
Db 480 GVVSLGNGAVLSYKNGTGDASNSITLKHIGLNLSSILKSGAEPLLWVEPTNNSNY 539
QY 541 TADTAATSLSDVLSLIDDDYNSPYESTDLTHALSSQPMLSISEASDNOLRSDMDDFSG 600
Db 540 TADTAATSLSDVLSLIDDDYNSPYESTDLTHALSSQPMLSISEASDNOLRSDMDDFSG 599
QY 601 LNVPHYGWGLWTGWAKTQDPEPASSATITDPQKANRPHRTLLTLWLPAGVYVSPKHS 660
Db 600 LNVPHYGWGLWTGWAKTQDPEPASSATITDPQKANRPHRTLLTLWLPAGVYVSPKHS 659
QY 661 PLIANTLGNMLLATSLKNSAELTPSDHPFWGITGGGLGMVYQDPRENHFGFHRSSG 720
Db 660 PLIANTLGNMLLATSLKNSAELTPSGHPFWGITGGGLGMVYQDPRENHFGFHRSSG 719
QY 721 YSAGMIAGOTHTFSLKFSQTYTKLERYAKNNVSKNYSCQGMFLSLQEGFLTLKLVL 780
Db 720 YSAGMIAGOTHTFSLKFSQTYTKLERYAKNNVSKNYSCQGMFLSLQEGFLTLKLVL 779
QY 781 YSYGHNCHHFTQGENLTSGTFRSQTMGGAVFEDLPKMPGSGTHILTAFLGALGIYS 840
Db 780 YSYGHNCHHFTQGENLTSGTFRSQTMGGAVFEDLPKMPGSGTHILTAFLGALGIYS 839
QY 841 SLUSHEVGAYPEPRSTKTPLNLVLPICVKGSEFMNATORQAWTVLAYQVLYRQBP 900
Db 840 SLUSHEVGAYPEPRSTKTPLNLVLPICVKGSEFMNATORQAWTVLAYQVLYRQBP 899
QY 901 IATQLLASKGIWFGSGSPSSRHMSYKISQQTQPLSWLTLHFQYHGFYSSSTFCNYLNGE 960
Db 900 IAAQLLASKGIWFGSGSPSSRHMSYKISQQTQPLSWLTLHFQYHGFYSSSTFCNYLNGE 959
QY 961 IALRF 965
Db 960 IALRF 964
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```
RESULT 2
F81722
Polymorphic membrane protein E/F family TC0261 [imported] - Chlamydia muridarum (strain
C:Species: Chlamydia muridarum, Chlamydia trachomatis MoPn
C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 11-May-2000
C:Accession: F81722
R:Read, T.D.; Brunham, R.C.; Shen, C.; Gall, S.R.; Heidelberg, J.F.; White, O.; Hickey,
C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg,
Nucleic Acids Res. 28, 1397-1406, 2000
A:Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.
A:Reference number: A81500; MUID:20150255; PMID:10684935
A:Accession: F81722
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-976 <TET>
A:Cross-references: GB:A8002293; GB:A8002160; NID:g7190298; PIDN:AAF39130.1; PID:g7190300
A:Experimental source: strain Nigg (MoPn)
C:Genetics:
A:Gene: TC0261
```

```
Query Match 71.7%; Score 3648.5; DB 2; Length 976;
Best Local Similarity 70.5%; Pred. No. 7.3e-216;
Matches 689; Conservative 121; Mismatches 154; Indels 13; Gaps 3;
QY 1 MKKAFFFLGNSLSGLAREVPSRIFLMPNSVPDPTKESLSNKISLTGDTNLTNLCYLDN 60
Db 1 MKKLEFFFLGSSILGFTREVPSPSILLAPILNPHVTGCLFPKPNLGLDTHNLNDYHLDN 60
QY 61 LRYLAILAQLQTPNEGAATITDYLSFFDTQKEGIFYFAKALNPESGGAIGYASPNSTVEI 120
Db 61 LKCILACLQRTPYEGAAFTVDYLGSDTQKDGIKFCFKNLNPESGSGVIGSPTQPTPIKI 120
QY 121 RDTGPIFENNTCCRPFTSSNPNNAVNKIREGGAIHAQNLYINHNHDVVGFMKNFSYVR 180
```

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Db 121 HNTGIPVLFENNTCHRLWTQTDPENEGKAREGGAIHAGDVVISNNQNLVGFKNFAYVQ 180
QY 181 GGAISTANTFVYSENOQSCFLFMDNTICIQNTAGKGAIIYAGTSNFSFNCDLFFINNAC 240
Db 181 GGAIS-ANTFAYKENKSSFLCLNNSCIQTKGKGAIYVSTSCSPENNKKOLLFTQNSG 239
QY 241 CAGGAIFSPICSLTGNRGNIYVNNRCFKNVETASSEASDGGAIKVTTRDLTVNRRFLP 300
Db 240 CAGGAIFSPICSLIQQGDIVFYSNHGFKNVDNATNESGDGGAIKVTTRDLITNNGSQIF 299
QY 301 FSDNITKNYGGAIYAPVVTVDNGPTFYFINNIANKGGAIIYIDGTSNKSISADRAIIIFN 360
Db 300 FSDNISRNFGGAIHAPCLHLVCGNGPTFYFINNIANKGGAIIYIDGTSNKSISADHAIIFD 359
QY 361 ENIVTNVNTANGTSANPPRRNAITVAVSSGEILLGAGSSQNLIIFYDIEVSNAGVSYS 420
Db 360 NNISANATNADGSSNTNPPHRNAITMDNSAGGIELGAGKSNLIIFYDIPQVNTAGVTVD 419
QY 421 FNKEADQTSVYFSGATVNSADFHORNLOTKTPAPLTLNSGFLCIEDHAQLTVNRFTQG 480
Db 420 FNKDSAQTCGVVFSGATVLSADISOANLOTKTPALTLTSHGLLCIEDRAQLTVNNTQFG 479
QY 481 GVVSLGNGAVLSYKNGAGN-----SASNASITLKHIGLNLSSILKSGAEPLLWVE 532
Db 480 GIVALGNGAVLSYQHSHTDATQTPPTTTTASVTLNHLGNLPSILKDGAEMLLWVE 539
QY 533 PTN----NSNNTADTAATSLSDVLSLIDDDYNSPYESTDLTHALSSQPMLSISEASD 588
Db 540 PISTTQGGTNTYTDAAASFSLNGATLSLIDEDGSPYENTDLSRALYAAQPMALASEAD 599
QY 589 NOLRDDDMDFSLGNPHYWGGLWTGWAKTQDPEPASSATITDPQKANRPHRTLLTLW 648
Db 600 NOLQSEMDFSKYNVPHYGWGLWTGWAKTENPTTTPATITDPPKANQFHTLLTLW 659
QY 649 PAGYVPSPKHSPLIANTLWGNMLLATSLKNSAELTPSDHPFWGITGGGLGMVYQDP 708
Db 660 PAGYIPSPKHSPLIANTLWGNILFATENLKNSSGOELLDPRFPWGITGGGLGMVYQEP 719
QY 709 ENHFGFHRSSYSGAMTAGOTHTFSLKFSQTYTKLERYAKNNVSKNYSCQGMFLSL 768
Db 720 KDHPGFHMTSGYSAGMITGNHTTSLRPSOSYTKLERYAKNNVSKNYSCQGMFLSL 779
QY 769 QEGFLTLKLVGLSYGDHCHHFTYQGENLTSGTFRSQTMGGAVFEDLPKMPGSGTHIL 828
Db 780 QEGLMLTKLIGLSYGNHSHHFTYQGEDLSQGEFHSQTTGGAVFDLPKPFGRTHIL 839
QY 829 TAPFLGALGIYSLSHFTVEVGAYPEPRSTKTPLNLVLPICVKGSEFMNATORQAWTV 888
Db 840 TAPFLGALGIYSLSHFTVEVGAYPEPRSTKTPLNLVLPICVKGSEFMNATORQAWTV 899
QY 889 AYQPVLYRQEPGIATOLLASKGIWFGSGSPSSRHMSYKISQQTQPLSWLTLHFQYHGF 948
Db 900 AYQPVLYRQEPGISITOLLAGKGMFPHGSPASRHALAYKISOKTQLLRPATLQLQYHGY 959
QY 949 SSSTFCNYLNGEIALRF 965
Db 960 SSSTFCNYLNGEVSILRF 976
```

```
RESULT 3
F86548
Polymorphic outer membrane protein E family [imported] - Chlamydia pneumoniae (st
C:Species: Chlamydia pneumoniae, Chlamydia pneumoniae
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 02-Mar-2001
C:Accession: F86548
R:Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.;
Nucleic Acids Res. 28, 2311-2314, 2000
A:Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.
A:Reference number: A86491; MUID:20330349; PMID:10871362
A:Accession: F86548
A:Status: preliminary
A:Molecule type: DNA
```

A;Residues: 1-938 <STO>
A;Cross-references: GB:BA000008; NID:g8978836; PIDN:BAA98772.1; GSPDB:GN00142
A;Experimental source: strain J138
C;Genetics: -
A;Gene: pmp_15

Query Match 22.0%; Score 1120.5; DB 2; Length 938;
Best Local Similarity 30.9%; Pred. No. 8.9e-61;
Matches 308; Conservative 163; Mismatches 418; Indels 109; Gaps 31;

QY 6 FFLIGNSLGLAREVPSRIFLPMNSVPDPTKESLSNKSILUTGDTNLT-----NC 56
DB 12 FTEVLAN--EGLQLPETYITLSPYQAAPQ-----VGFTNQNDLAIVGNHND 59
QY 57 YLNLRLVILAILKPTNEGAAVITDYLSPFDQKEGIVFAKNLTIPSAGGAIYASPNP 116
DB 60 FILDYKY-----RSNGALCKNLL--ISENIGNVFKEKNCVPSGGAI-YAQN- 108
QY 117 TVEIRDTIGVIFENNTCCRPFTSSNPNAAVNKIREGAIHAQNLYINHHNDVVGPMKNF 176
DB 109 -----TISK--NONVAFNTLVSDNPTATAGSLL--GGALFAINCSTINNLGQGTFFVDNL 159
QY 177 SYVRGAISTANTFVYSENGSCFLFMDNICIQNTAGKGAIIYAGTNSFESNCDLFFI 236
DB 160 ALNKGALYETETNLSIKDNKGPITIKONRAL--NSDSLGGIYSGNSLTNEGSAIQIT 217
QY 237 NNACCGAGALFS-PICSLTGNRGNIVFYNNRCFKNVETASSEASDGAIAKVTTRLDVTGN 295
DB 218 SNSGSGGGIFSTQTLTISNNKLLIESENSAFAN--NYGSNFPGGGGTTFTCILNN 275
QY 296 RGRIFTSNDITNKYGAIYAPVVTLDNGPTYFINNIANNKGAIIYD-GTNSK--ISA 352
DB 276 REGVLENNQSQNGGAIHAKSIIKENGPPVFLNNTATRGGALLNLSAGSGNGSFTLSA 335
QY 353 DRHAIIFENIVNTVNGTSTSANPPRNAITVASSGCEILLGAGSSONLIFYDPIEV 412
DB 336 DNGDIIFNNN-----TASKHALNPPYRNAIH-STPNMNLQIGARPGYRVLYFDPIEH 386
QY 413 S-NAGVSVSFNKADQTSVVFSGATVNSADFHORNLOTKTPAPLTLSNGFLCIEDHAOL 471
DB 387 ELPSSPILFNTGTGTGVLFSGEHVHQNFTDEMFFYLRNTSELRQGVLAIVEDAGL 446
QY 472 TVNRFTQTGGVSLGNGAVLSCYKNAGN-----SASNASITLKHGLNLSILKSG 523
DB 447 ACYKFFQGGTLLGGQAVIT--AGTIPTSPSTTVGSTITLNHIAIDLPSILSFQ 502
QY 524 AEIPLWVEPTNNSNYTADTAATFSLDSVKLSLIDYGNPSYESTDLTHALSQPMLSI 583
DB 503 AQAPKIWIYPTKGTSTYTEDSNPTITISGT-LTLRNSNEDPYDLSLDLSHLEKVPLLYI 561
QY 584 SEASDNLQRDDMDFSGLNV-PHYGQGLWTGWAKTQDPEPASSATITDPQK---ANRF 639
DB 562 VDVAQKINSQDLSTLNGEHYGQGIWSTYTWET-----TTITNPTSLLGANTK 613
QY 640 HRTLLTLWPAGVVPSPKPHRSPLIANTLWGNMLLATLESKNSELTSPSDHPFWGITGG-- 697
DB 614 KLLLYANWSPGLYRPHRPERGEITNALWQSAYTALAGLSLS-----WDEKGA 665
QY 698 ----GLGMVYQDPRENHPGFHMRSSGYSAGMTA--GQHTFSLKFSQYTKLNERYAKN 751
DB 666 ASLQIGLLVHQDKNGFKGFRSHMTGYSATTEATSSQSPNFSILGFAQFFSKAKEHSQN 725
QY 752 NVSSKNY---SCOGEMFLSLQEGFLTKVLGL--YSYGDHNCHEFFYQGENLTSGQFRSQ 807
DB 726 STSHHFTSGMCIENTLF--KEWIRUS--VSLAYMTSEHTHTMYOGLLEGNSQGSFHNH 781
QY 808 TMGAVFFDLPMKPFPGSTHLLTAPFALGAIYSSLSHFTEVGAYPRSFSTKPLINVLVP 867
DB 782 TLGALSCLVLPQPHGES-LQIYFFITAIIRGNLAFAQESGDHAREFSLHRPLTDVSLP 840
QY 868 IGKVGFMNATQRPQAWTVELAYQPVLYRQEPGIATQILASKGIWFGSGSPSSRHAMSYK 927
DB 841 VGRISWKNHHRVPLVWLTEISYRSTLYRODPELHSLKLLISQGTWTWTQTPVPTYNALGIK 900

QY 928 ISQOTQPLSLMTLHFQYHGFSSTFCNLYNLGEIALRF 965
DB 901 VKNTMQVFPKVTLSLDYSADISSSTLSHYLNVASRMRF 938
RESULT 4
H72074
polymorphic membrane protein E/F family CP0286 [imported] - Chlamydomphila pneumoniae
C;Species: Chlamydomphila pneumoniae, Chlamydia pneumoniae
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 11-May-2000
C;Accession: H72074; E81593
R;Kallman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, Nature Genet. 21, 385-389, 1999
A;Title: Comparative genomes of Chlamydia pneumoniae and C. trachomatis.
A;Reference number: A72000; MUID:99206606; PMID:10192388
A;Accession: H72074
A;Molecule type: DNA
A;Residues: 1-938 <ARN>
A;Cross-references: GB:AE001631; GB:AE001363; NID:g4376750; PIDN:AAD18608.1; PID:g437
A;Experimental source: strain CWL029
R;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hicke, C.; Dodson, R.; Gwinn, M.; Neilson, W.; DeBoy, J.; Kolonay, J.; McClarty, G.; Salzbe Nucleic Acids Res. 28, 1397-1406, 2000
A;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39
A;Reference number: A81500; MUID:20150255; PMID:10684935
A;Accession: E81593
A;Molecule type: DNA
A;Residues: 1-938 <REA>
A;Cross-references: GB:AE002190; GB:AE002161; NID:g7189209; PIDN:AAF38143.1; PID:g718
A;Experimental source: strain AR39, HL cells
C;Genetics:
A;Gene: pmp_15; CP0286

Query Match 22.0%; Score 1120.5; DB 2; Length 938;
Best Local Similarity 30.9%; Pred. No. 8.9e-61;
Matches 308; Conservative 163; Mismatches 418; Indels 109; Gaps 31;

QY 6 FFLIGNSLGLAREVPSRIFLPMNSVPDPTKESLSNKSILUTGDTNLT-----NC 56
DB 12 FTEVLAN--EGLQLPETYITLSPYQAAPQ-----VGFTNQNDLAIVGNHND 59
QY 57 YLNLRLVILAILKPTNEGAAVITDYLSPFDQKEGIVFAKNLTIPSAGGAIYASPNP 116
DB 60 FILDYKY-----RSNGALCKNLL--ISENIGNVFKEKNCVPSGGAI-YAQN- 108
QY 117 TVEIRDTIGVIFENNTCCRPFTSSNPNAAVNKIREGAIHAQNLYINHHNDVVGPMKNF 176
DB 109 -----TISK--NONVAFNTLVSDNPTATAGSLL--GGALFAINCSTINNLGQGTFFVDNL 159
QY 177 SYVRGAISTANTFVYSENGSCFLFMDNICIQNTAGKGAIIYAGTNSFESNCDLFFI 236
DB 160 ALNKGALYETETNLSIKDNKGPITIKONRAL--NSDSLGGIYSGNSLTNEGSAIQIT 217
QY 237 NNACCGAGALFS-PICSLTGNRGNIVFYNNRCFKNVETASSEASDGAIAKVTTRLDVTGN 295
DB 218 SNSGSGGGIFSTQTLTISNNKLLIESENSAFAN--NYGSNFPGGGGTTFTCILNN 275
QY 296 RGRIFTSNDITNKYGAIYAPVVTLDNGPTYFINNIANNKGAIIYD-GTNSK--ISA 352
DB 276 REGVLENNQSQNGGAIHAKSIIKENGPPVFLNNTATRGGALLNLSAGSGNGSFTLSA 335
QY 353 DRHAIIFENIVNTVNGTSTSANPPRNAITVASSGCEILLGAGSSONLIFYDPIEV 412
DB 336 DNGDIIFNNN-----TASKHALNPPYRNAIH-STPNMNLQIGARPGYRVLYFDPIEH 386
QY 413 S-NAGVSVSFNKADQTSVVFSGATVNSADFHORNLOTKTPAPLTLSNGFLCIEDHAOL 471
DB 387 ELPSSPILFNTGTGTGVLFSGEHVHQNFTDEMFFYLRNTSELRQGVLAIVEDAGL 446
QY 472 TVNRFTQTGGVSLGNGAVLSCYKNAGN-----SASNASITLKHGLNLSILKSG 523
DB 447 ACYKFFQGGTLLGGQAVIT--AGTIPTSPSTTVGSTITLNHIAIDLPSILSFQ 502

Db 769 E-QAGTCYSHTLAAAGCGFFWQKQSYLHL--SPFVQAIATRSHTAFEEIGDGNPRKFV 825
QY 857 TKTPLINVLPIGVKSGFNMNATQRPQAWTVLAYOPVLYRQBPQIATQLLASKGIWFGSG 916
Db 826 SOKPFYNLTPLIGIQKQSKFHVTEWTLSELYOPVLYQONPQIGVILLASGGSDIILG 885
QY 917 SPSSRHMSYKISQOTQPLSWLTLHFQYHGFYSSSTFCNYLNGEIALRF 965
Db 886 HNYVRNALGYKHNOTALFRSLDLFLDYQGSVSSSTHTHLQAGSTLKF 934

RESULT 8
C86549
polymorphic outer membrane protein E/F family [imported] - Chlamydothila pneumoniae (std
C:Species: Chlamydothila pneumoniae, Chlamydia pneumoniae
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 02-Mar-2001
C:Accession: C86549
R:Shiral, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; Is
Nucleic Acids Res. 28, 2311-2314, 2000
A:Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.
A:Reference number: A86491; MUID:20330349; PMID:10871362
A:Accession: C86549
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-946 <STO>
A:Cross-references: GB:BA000008; NID:98978841; PIDN:BAA98677.1; GSPDB:GN00142
A:Experimental source: strain J138
C:Genetics:
A:Gene: pmp_18

Query Match 18.7%; Score 951.5; DB 2; Length 946;
Best Local Similarity 29.1%; Pred. No. 2.1e-50;
Matches 281; Conservative 168; Mismatches 416; Indels 101; Gaps 34;

QY 35 PTKESLSNKISLTGDTHNLT-----NCYLDNRYLAILQKTPNEGAIVTIDYL 84
Db 47 PLIDLTN---WTPYSHRATLFGVRDDNQDIVLDHONSIESWFENFSDGGALSKS-L 102
QY 85 SFDDTKQEGYFAKNLTPESGAIGYASPNPTVEIOTIGVPIENNTCCRPFTSSNP 144
Db 103 AITNT-KNOILFLNSFAIKRAGM-YVNGN---FDLSENHGSIIIFSGNL-----SPFN 150
QY 145 AA--VNKIREGAIHAQNLINHHNDVVGFMKNFSYRGGAISTANTVFNENQSCFLFM 202
Db 151 ASNFADTCGGAVLCSKNVTISKNOGTAYFINNKAQSGGAIQAAIINIKDNTGCLFF- 209
QY 203 DNICITQTAG--KGAIIYAGTNSFESNCDLFPINNACAGGAI-FSPICSLTGNRN 259
Db 210 -----NNAAGTAGGALFANACR-IENNSQPIYFLNNSQGLGGAIRVHQECILTKNTGS 262
QY 260 IVFYNNRCFKNVEITASSEASDGAIKVTRLDVTCNRRGRIFFSDNITKNYGAIVPVVT 319
Db 263 VIFNHN--FAMEADISANHSSGGAIYICIS-CSIKDNPQIAAFDNTAARDGAICTQSLT 319

Query Match 18.7%; Score 951.5; DB 2; Length 946;
Best Local Similarity 29.1%; Pred. No. 2.1e-50;
Matches 281; Conservative 168; Mismatches 416; Indels 101; Gaps 34;

QY 35 PTKESLSNKISLTGDTHNLT-----NCYLDNRYLAILQKTPNEGAIVTIDYL 84
Db 47 PLIDLTN---WTPYSHRATLFGVRDDNQDIVLDHONSIESWFENFSDGGALSKS-L 102
QY 85 SFDDTKQEGYFAKNLTPESGAIGYASPNPTVEIOTIGVPIENNTCCRPFTSSNP 144
Db 103 AITNT-KNOILFLNSFAIKRAGM-YVNGN---FDLSENHGSIIIFSGNL-----SPFN 150
QY 145 AA--VNKIREGAIHAQNLINHHNDVVGFMKNFSYRGGAISTANTVFNENQSCFLFM 202
Db 151 ASNFADTCGGAVLCSKNVTISKNOGTAYFINNKAQSGGAIQAAIINIKDNTGCLFF- 209
QY 203 DNICITQTAG--KGAIIYAGTNSFESNCDLFPINNACAGGAI-FSPICSLTGNRN 259
Db 210 -----NNAAGTAGGALFANACR-IENNSQPIYFLNNSQGLGGAIRVHQECILTKNTGS 262
QY 260 IVFYNNRCFKNVEITASSEASDGAIKVTRLDVTCNRRGRIFFSDNITKNYGAIVPVVT 319
Db 263 VIFNHN--FAMEADISANHSSGGAIYICIS-CSIKDNPQIAAFDNTAARDGAICTQSLT 319

QY 608 WOGLTWGAKTQDPEPASATITDPQKANRPHRTLLTLWLPAGYVSPKPHRSPLIANTL 667
Db 597 YGVWSPYWIETITTSDFSS-----EDVTNLTLRQLYGDWTPGTGYKVNPKNGDIALSAF 651
QY 668 W---CNMLLATESLNSAELPSPDHFWGITGGGGLGMVYQDPRENHGFHMRSSGYSAG 724
Db 652 WQSFNLFATLRYOTQOQGIAPT-----ASGEATRLFVHQNSNDKAGFHEATGYSLG 705
QY 725 MIA--GQTHFSLKFSQTYTKLNERYAKNNVSKNYSQOGEMLFS-LOGGFLLTLKLVLGY 781
Db 706 TTSNTASHNSGCVNFSQLFSLNLYESHSDNSVASHTTTVALQINNFWLQERFSTASLA-Y 764
QY 782 SYGDHNCHEFTQGEN--LTSQGTFSQTMGGAVFDFLPMKPFPGSTHILITAPFALGALGY 839
Db 765 SYSN---HHIRASGYSGIKQTEGKCYSTTLGAALSCSLSLQ-WRSRPLHFTFPIQAIAR 820
QY 840 SLSHTEVGAVPRFSFKTPLINVLPIGVKSGFMNATQRPQAWTVLAYOPVLYRQBP 899
Db 821 SNOTAFQESGDKARKFSVHKPLYNLTPLIGIQSAWESKFRPLTYWNIELAYOPVLYQNP 880
QY 900 GIATOLLASKGIWFGSGSPSSRHMSYKISQOTQPLSWLTLHFQYHGFYSSSTFCNYLNG 959
Db 881 EVNVSLESGSWLLSGTTLARNATAFGRNQIIFPKLSVFLDYQGSVSSSTTTTHYLHA 940
QY 960 EIALRF 965
Db 941 GTTFKF 946

RESULT 9
D81594
polymorphic membrane protein E/F family CP0283 [imported] - Chlamydothila pneumoniae
C:Species: Chlamydothila pneumoniae, Chlamydia pneumoniae
C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 11-May-2000
C:Accession: D81594
R:Read, T.D.; Brumham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hicke
C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzbe
Nucleic Acids Res. 28, 1397-1406, 2000
A:Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39
A:Reference number: A81500; MUID:20150255; PMID:10684935
A:Accession: D81594
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-946 <REA>
A:Cross-references: GB:AF002189; GB:AE002161; NID:97189205; PIDN:AAF38141.1; PID:9718
A:Experimental source: strain AR39, HL cells
C:Genetics:
A:Gene: CP0283

Query Match 18.7%; Score 951.5; DB 2; Length 946;
Best Local Similarity 29.1%; Pred. No. 2.1e-50;
Matches 281; Conservative 168; Mismatches 416; Indels 101; Gaps 34;

QY 35 PTKESLSNKISLTGDTHNLT-----NCYLDNRYLAILQKTPNEGAIVTIDYL 84
Db 47 PLIDLTN---WTPYSHRATLFGVRDDNQDIVLDHONSIESWFENFSDGGALSKS-L 102
QY 85 SFDDTKQEGYFAKNLTPESGAIGYASPNPTVEIOTIGVPIENNTCCRPFTSSNP 144
Db 103 AITNT-KNOILFLNSFAIKRAGM-YVNGN---FDLSENHGSIIIFSGNL-----SPFN 150
QY 145 AA--VNKIREGAIHAQNLINHHNDVVGFMKNFSYRGGAISTANTVFNENQSCFLFM 202
Db 151 ASNFADTCGGAVLCSKNVTISKNOGTAYFINNKAQSGGAIQAAIINIKDNTGCLFF- 209
QY 203 DNICITQTAG--KGAIIYAGTNSFESNCDLFPINNACAGGAI-FSPICSLTGNRN 259
Db 210 -----NNAAGTAGGALFANACR-IENNSQPIYFLNNSQGLGGAIRVHQECILTKNTGS 262
QY 260 IVFYNNRCFKNVEITASSEASDGAIKVTRLDVTCNRRGRIFFSDNITKNYGAIVPVVT 319
Db 263 VIFNHN--FAMEADISANHSSGGAIYICIS-CSIKDNPQIAAFDNTAARDGAICTQSLT 319

[illegible]

RESULT 10
C72075
polymorphic outer membrane protein e/f family - Chlamydothrix pneumoniae (strain C72075)
C:Species: Chlamydothrix pneumoniae, Chlamydothrix pneumoniae
C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 05-May-2000
C:Accession: C72075
R:Kalan, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, J.;
Nature Genet. 21, 385-389, 1999
A:Title: Comparative genomes of Chlamydothrix pneumoniae and C. trachomatis.
A:Reference number: A72000, MUID:99206606; PMID:10192388
A:Accession: C72075
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-946 <ARN>
A:Cross-references: GB:AE001631; GB:AE001363; NID:g4376750; PIDN:AAD18610.1; PID:g4376750
A:Experimental source: strain C72075
C:Genetics:
A:Gene: pmp_18

Query Match 18.6%; Score 948.5; DB 2; Length 946;
Best Local Similarity 29.1%; Pred. No. 3.2e-50;
Matches 281; Conservative 167; Mismatches 417; Indels 101; Gaps 34;

RESULT 11
F71460
probable outer membrane protein F - Chlamydia trachomatis (serotype D, strain UW3/Cx
C:Species: Chlamydia trachomatis

C>Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 08-Oct-1999
C:Accession: F71460
R:Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell,
Science 282, 754-759, 1998
A:Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia tra
A:Reference number: A71570; MUID:99000809; PMID:9784136
A:Accession: F71460
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1034 <ARN>
A:Cross-references: GB:AE001360; GB:AE001273; NID:g3329342; PIDN:AAC68468.1; PID:g332934
A:Experimental source: serotype D, strain UW-3/Cx
C:Genetics:
A:Gene: pmpF

Query Match 17.0%; Score 866.5; DB 2; Length 1034;
Best Local Similarity 28.1%; Pred. No. 3.9e-45;
Matches 293; Conservative 149; Mismatches 406; Indels 193; Gaps 36;
QY 55 NCYDMLRILAILQKTPNEGAATITDYLSPFDQKEGIYFAKNLTPESGGAI----- 108
DB 57 NIVLSNLQ-----SNGTGACTISG-----NTQTIFSNVNTADSGGAFDMVWTS 102
QY 109 -----GYASPNPTVEIRDITGPIVFENNTCCRPFTSSNPAAV-----NK 149
DB 103 FTASDNALLFCNNYCTHKNKGGAIRSG-GPIRFLNNQDVLFFYNNISAGAKYVGTGDHNE 161
QY 150 IREGGAIHAQNLINNHVDVGMKNSFYVVGGAISTANTFVSENQSCFLFDNLCI-- 207
DB 162 KNRGGALYATITLTGNR-TLAFINMSGDCGGAISADTQISTDPTVKILFENNHTLNH 220
QY 208 ----QNTAGKGAIVAGTS-NSFESNCCDLFFINNACCAGGAIFSPICSLTGNRGNIVF 262
DB 221 IPTQAEENMARGAICRRDLCSISNNSGPIVENYNOGKGGAISATRCVIDNKRERIF 280
QY 263 YNNRCFKNVETASSEASDGAIVKTRLDVTGNRGRIFPSDITNKYGAIVAPVVTLVD 322
DB 281 SNNSLSG--WSQSSASNGGAITQQTGFTLRNKGSIYEDSNTATHAGGAINCGYDIDR 338
QY 323 NGPTPIFINNANKGAIYIDGTSKISADRA-----IIFENIVNTVNTNANG 372
DB 339 NGPVVFLNNSA--AMGAAB-----NLSKPSATNYIHGTGDIVFNFNVTLDGNLL 389
QY 373 TGTSAAPPRRNAITVASSSGEILLGAGSSQNLIFYDPIE-----VSNAGVS-----V 419
DB 390 GRKLFHINNETPTLS---LGAKKTRIVFYDYLFWERKENTSNPPSPTRNTI 445
QY 420 SENKEADQTSVVFSGATVNSADFHORNQTK-----TPAPLTSLNGFLCIEDHAQLTVN 474
DB 446 TVNPETESGAVVFS---YNQMSSDIRTLGMKEHNYIKEAPTTLKFGTLAIEDDAELEIF 502
QY 475 R--FTOT-GGVVSGLNGAVLSCYKNGAGNASNASTTLKHGILNSSLILSKAEIPLLMV 531
DB 503 NIPFTQNPISLLAGSGATLVKGKG-----KLNIITNLGVIPIILKEKSGPPCIRV 554
QY 532 EPTN-NSNNYTADT-AAFTSL-----DVKLSLDDYDGNPSYESTDLTHALSSQPMLSI 583
DB 555 NPQDMTQNTGTQTPSSSTSSITPMIIFNGRLSIVDENYESYDSDLSRGAELIILSI 614
QY 584 SEASDNQLRSD--DWDPSGLNVPHYGWGLTWGWAKT-----QDPEPASSATITD 632
DB 615 EFTNDQGLSDNSQSSSLNTSLLSPHYGQGLWTPNMTITTYITLNNSSAPTSAISAE 674
QY 633 POKANR-----PHTLLLTWLPAGYVPSPKH 658
DB 675 QKKTSETTPSNWTASTIPNIKASAGSGSGSASNSGEVITKHTLVVWAPVGYIVDPIR 734
QY 659 RSPLIANTL--WGNMLLATESLKNSAELTPSDHPFWGITGGGLGMVYQDPRENHPGFH 715
DB 735 RGDLIANSLVHSGRNTMGLRSL-----PDNSWEALOGAATTLFTKQKRLSVHGVY 787
QY 716 MRSSGYSAGMIA--QOHTFSLKFSQTYTKLNERVAKNVSSKNY-----SCQGEMLFSQE 770

DB 788 SASKGYTVSSQASGAHGHKFLLSFSQSSDKMKEKETNNRLSSRYLUSALCFEHPMPD--- 844
QY 771 GFLLTKLVG--LVSYGDHNCHEHYTOGENLTSQGTFRSOTMGGAVFEDL---PMKPFGS 824
DB 845 ---RIALIGAAACNVTGTHNRGFY--GTRKSSKGKPHSTTLGASLCELRDSMPLR---- 895
QY 825 THILTAPFLGALGIYSSLSHFTEVGAYPRSFRTKPLINVLPIGIVKGFSFMNATORQAW 884
DB 896 -SIMLTPFAQALFSRTEPASIRESGDLARLFLEQAHTAVVSPIGIKGAYSSDTWPTLSW 954
QY 885 TVELAYQPVLYRQEPGIATOLLASKIWFSGSPSRHAMSYSKISOOTPLSLWTLHFY 944
DB 955 EMELAYQPTLYWKRPILLNTLLIQNNGSWVTINTPLAKHSF-YGRGSHSLKFSHLKLFANY 1013
QY 945 HGFYSSSTFCNVLNGEIALRF 965
DB 1014 QAEVATSTVSHYNAGALVF 1034
RESULT 12
G81722
polymorphic membrane protein E/F family TC0262 [imported] - Chlamydia muridarum (stra
C:Species: Chlamydia muridarum, Chlamydia trachomatis MoPn
C>Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 11-May-2000
C:Accession: G81722
R:Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heideberg, J.F.; White, O.; Hicke
Nucleic Acids Res. 28, 1397-1406, 2000
A:Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39
A:Reference number: A81500; MUID:20150255; PMID:10684935
A:Accession: G81722
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1025 <TET>
A:Cross-references: GB:AE002293; GB:AE002160; NID:g7190298; PIDN:AAF39131.1; PID:g719
A:Experimental source: strain Nigg (MoPn)
C:Genetics:
A:Gene: TC0262
Query Match 15.6%; Score 793; DB 2; Length 1025;
Best Local Similarity 27.0%; Pred. No. 1.3e-40;
Matches 269; Conservative 158; Mismatches 419; Indels 152; Gaps 35;
QY 68 LOKTPNEGAATITDYLSPFDQKEGIYFAKNLTPESGGAIVASPNSPTEIRDTIGV 127
DB 80 LSTTSSGAFV--ESMTSETADNADLFCNNYCTHOGG--GGAINATGLISFKNNQNL 135
QY 128 IFENNTCCRPFTSSNPNAAVNKIREGGAITHAQNLINNHVDVGMKNSFYVVGGAISTA 187
DB 136 FYNNTTTIGTQGTGVALRTERNR--GGALYSSSIELINNHS-LNFINTSGDMGGAVSTI 191
QY 188 NTFVVSQSCFLFDNLCIQ--TWT---ACKGGAIVAGTSNSFESNCCDLFFINNACC 241
DB 192 QNLVKNSTSGIVAFENNNHTDHPNPTFATILARGGAVGCGACETSHNTGPVVFVNSYGG 251
QY 242 AGGAIFS-PICSLTGNRGNIVFNRRKFNKVTASSEASDGAIVKTRLDVTGNRGRIF 300
DB 252 YGGAISTGQCIFRDKDKLIFINNSALGWHNT--SAQNGAVISAGGEFGLNKNKGPY 309
QY 301 FSDNTKNGYGAIVAPVTVLDVNGPTYPINNTANNKGAIVYIDGT-SNSKISADRAIIF 359
DB 310 FENNNASYIAGAISSCNLNLFQENGPIYFLNNSA-LYGGAFHLFASPAANYIHGSGDIIF 368
QY 360 NENIVNTVNTAN-----GTSTSANPPRRNAITVASSSGEILLGAGSSQNLIFYDP 409
DB 369 NNTELTSTGMSAGURKLFYIPGTNN-----NPITLS-----LGAKKTRIVFDL 415
QY 410 IE-----VSNAGVSVFENKEADQTSVVFSGATVNSADFHORNQTKT-----PA 454
DB 416 FQWGLKKNANTPPENSPHTVITNPSDEFSGAVVSYKNI-SSDLQAHMTASKTHNQKDS 474
QY 455 PTLTSLNGFLCIEDHAQ-----LTVNRTQTVGGVSLNGAVLSCYKNGAGNASNASI 507

Db 475 PTLKFGTMSIENGAEFEFFNGPLT-----OESTSLLALGQDSILTGVK-----DASL 522
QY 508 TLKHIGLNSILK-SGAELPLWVEP---TNSNNYATADTAATFSLSDVKL-----SL 557
Db 523 TITHLGIPLCLNDGQTAPRIRVNPQMTQNTNQA-PVSTENATQKIEFFSLVSL 581
QY 558 IDYGNPSYESTDLTHALSSQPMLSISEASDNLRSD---DMDFGSLNVPHYGQGLWTW 614
Db 582 VDENEYSVDCSLSRGKANQPIHETITNDQSLNDKWNKTLNTSLYSLPHYGQGLWTS 641
QY 615 GWAKTODPEPASSATITDQKANR----- 638
Db 642 NMWT---TRTVSTNSETQTANNSIQEQKNTSETDSNSTTTAKIPSIRASTGGTPLA 699
QY 639 -----FHRTLTLTWLPAGVVPKPKRSPLIANTLGNMLLATESLKNSAELPSPDHPFW 692
Db 700 TTDVTVTRSLVSWPPIGVIADPARRGDLIANNLVSSGRNTLYLRS-----LLPDD-SWF 755
QY 693 GITGGGLGMVYQDPRENHGFHMRSGY---SAGMIAGQTHFTSLKFSQTYTKLNERIYAK 750
Db 756 ALQGSAAITFTKQKRLDYHGYSSASKGYAISQASGAHGHKFLFSFSQSSDMMKEKRTN 815
QY 751 NNYSNNYSCQEMLSLQEGFLITLVG---LYSYGDHCHHFTYTOGENLTSQTFERSQT 808
Db 816 NKISSRYL---SALCFEQPMFDRIALIGAAAYNYGTHKTYNFY---GTRKFSKGNFHSIT 870
QY 809 MCGAVFFDL-PMKPPFGSTHILTAPFLGALGIYSSLSHFTVEGAYPRSFSTKTLINVLVP 867
Db 871 LGSGLCELRLDSWPFOS---IMLTPFTQALISRTPEASIQEQDLARLFLSKQPHAVVSP 928
QY 868 IGKVSFMNATORQAWTVELAYQPVLYROEPCIATQLLASKGIWFGSPSSRHSAMSYK 927
Db 929 IGIKGVSSNKWPTVCEMVAQPTLYMKRPILNTVLKNGSWETNTPLAKHSF-YG 987
QY 928 ISQOTPLSWLTHFOYHGFYSSTFCNYLNGEIALRF 965
Db 988 RGSLLKFLYKLFANYQAQVATVTSVSHVMNAGGALVF 1025
RESULT 13
G71460
probable outer membrane protein G - Chlamydia trachomatis (serotype D, strain UW3/Cx)
C:Species: Chlamydia trachomatis
C:Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 08-Oct-1999
R:Accession: G71460
R:Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell,
Science 282, 754-759, 1998
A:Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia tra
A:Reference number: A71570; MUID:99000809; PMID:9784136
A:Accession: G71460
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1013 <ARN>
A:Cross-references: GB:AE001360; GB:AE001273; NID:g3329342; PIDN:AAC68469.1; PID:g332934
A:Experimental source: serotype D, strain UW-3/Cx
C:Genetics:
A:Gene: pmpG

Query Match 12.9%; Score 655.5; DB 2; Length 1013;
Best Local Similarity 25.7%; Pred. No. 3.4e-32;
Matches 261; Conservative 152; Mismatches 388; Indels 213; Gaps 43;
QY 39 SLSNKLSTGCDTHNLNLCYLDNLRIYLAILQKTPNCGAAVTIDYLSFFDTQKEGIFYAK 98
Db 84 NLIGSTFVLGRGHSLT---FENIR-----TSTNGAALS-----DSANSGLF--- 121
QY 99 NLTPESGGAIGYASPNSTVEIRDITGPVFENNTCCRPPTSNP-NAAV----- 147
Db 122 --TIEGFKELSFNCNSLLAVL-----PAAITNGSQTPITTSPTNGIYKSTIDLLLN 174
QY 148 -----NKIR-EGGAIHAQNLINHNHDVGVGMKNFSYVRGGAISTANTFVYVENQSC 198
Db 175 NEKFSFVSNLVSDGGDAIDAKSLTVQGISKLCVQENTAQADGACQVTSFSAMANEAP 234

QY 199 FLFMDNICIQTNTAG-KGGAIYA-----GTSNSFE-----SNNCDLFEFTINNACCAG 243
Db 235 IAFIANV-----AGVGGGIAAQQGQQQVSSSTSTEDPVVVSFRNTAVFEDGNVARG 288
QY 244 GAIFSPICSLTGNRGNIVFYNN--RCFKN-----VETASSASDGGAI 284
Db 289 GGIYS-----YGNVAFNLNGKTLFLNNVASPVYIAAEQPTNGQASNTSDNYGDDGAI 340
QY 285 KVTTRLDVTGN-----RCRIFFSDNITKNYGGAIYAPVVTLVLDNGPYTFINNAN 334
Db 341 FCKNGAQAAGSNNSGVSEDFGEGVFFSSNVAAGKGGAIYAKKLSVANCQPVQFLGNAN 400
QY 335 NKGGAIIIDGTSNKSISADRHAIIFNENI-----VTNVNANGTSTSANPPRRNAIVASS 390
Db 401 D-GGAIYLGESGELSADYGDIIIFGNLKRKTAKEADVNGVTVSS-----QAISWGS 454
QY 391 SGBILGASSQNLIFDYPIEVSN-----AGVSYSFNKEADQTSVVSFGATVNSADF 443
Db 455 GKITTIRAKAGHOILEFNDPIEMANGNNQPAQSEPLKINDGEGYTGDIVF--ANGNSTLY 512
QY 444 HORNLOTKPAPLTLNSGFLCIEDHAQLTVNRETQTVGVVSLGNGAVLSYCKNAGNS-- 501
Db 513 QN-----VTIEQGRIVLREKAKLSVNSLSQTSGLYMEAGSTLDFVTPQPPQPP 562
QY 502 ASNASITLKHIGLNSILKSGAEIPLWVEPTN--NSNNYATADTAATFSLSDVKLS--- 556
Db 563 AANQLITLNLHLSSLNLANNA---VTNPPTNPAQDSHPALIGST-TAGSVTISGPI 617
QY 557 LIDDYNSPYESTD-----LTHALSSQPMLSISEASDNQLRSDMDDFSLNVPHY 606
Db 618 FFEDLDDBTAYDRYDWLGSNOKIDVLKQLGCTQP--SANAPSDLTL-----GNEMPKY 667
QY 607 GWQGLTWGWAKTQDPEPASSATITDQKANRPHRTLLTLWLPAGVVPKPKHSPLIANT 666
Db 668 GYOGSWKLAW-----DPNTANNNGPYTLKATWTGTGYNPGPERVASIIVPNS 712
QY 667 LWCNMLLATESLKNSAELPSPDHPFW-GITGGGLGMVYQDPRENHGFHMRSGYSAGM 725
Db 713 LAGS-ILDIRSAHSAIOASVDGRSYCRGLWVSGVSNFFYHDIRDALCGQYRISGGYSLG- 770
QY 726 IAGQTHFTSLKFSQTYTKLNERIYAKNV--SSKNYSQCEMFLSLOEGFLTLKVLGLYSY 783
Db 771 --ANSYFGSSMFLGATFVEGR-SKDYVVCRSNHHACIGSVYLSLTKQA-----LCGSYLF 822
QY 784 GDHNCHEFTQ-ENLTSQTFERSQT-----MCGAVFFDLPMKPPFGSTHILT--APF 832
Db 823 GDATIRASYGFGNQHKMTSYTFAESDVRWDNCLVGEIGVGGLPIVITPSKLYLNELRPF 882
QY 833 LGALGIYSSLSHFTVEGAYPRSPSTKTLINVLVPIGVKSGFEMNATORQAWTVELAYQ 892
Db 883 VQAEFSYADHESFTEGDDQARAPRS-GHLMNLSVPVGVAFDRCSST-HPNKTSFMCAYIC 940
QY 893 VLYRQEPGIATQLLASKGIWFGSGSPSSRHSAMYSKISQOTQPLSWLTHFOYHG 946
Db 941 DAYRTISGQTTLTLLSHQETWTTDAFLARHGVIIVRGSMVAS-----LTSNIEVYG 990

RESULT 14
C72078
polymorphic outer membrane protein g family - Chlamydia pneumoniae (strain CWL029)
C:Species: Chlamydia pneumoniae, Chlamydia pneumoniae
C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 15-Jun-2001
R:Accession: C72078
R:Kalman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood,
Nature Genet. 21, 385-389, 1999
A:Title: Comparative genomes of Chlamydia pneumoniae and C. trachomatis.
A:Reference number: A72000; MUID:99206606; PMID:10192388
A:Accession: C72078
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-936 <ARN>
A:Cross-references: GB:AE001627; GB:AE001363; NID:g4376721; PIDN:AAD18589.1; PID:g437

